



STIC SEARCH RESULTS

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Questions about the scope or the results of the search? Contact *the searcher or contact*:

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

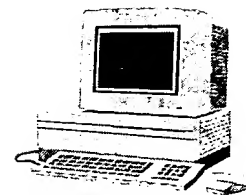
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BioTech-Chem Library

Search Results

Feedback Form (Optional)



Scientific & Technical Information Center

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 308-4258
CM-1 Room 1E01

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Other Comments:

Drop off completed forms at the **Circulation Desk CM-1**, or send to Mary Hale, CM1-1E01 or e-mail mary.hale@uspto.gov.

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 8, 2003, 07:47:00 ; Search time 23 Seconds
(without alignments)
1425.297 Million cell updates/sec

Title: US-09-401-636-4
Perfect score: 1958
Sequence: 1 EFMHHHTLSLPESGPVTI.....HEALPGSRTLEKSLHYSAGN 341

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1051	56.6	429	1 EHRT	Ig epsilon chain C
2	940.5	50.6	388	1 EHMS	Ig epsilon chain C
3	871.5	46.9	548	2 S28864	Ig epsilon chain C
4	862.5	46.4	423	1 EHMS	Ig epsilon chain C
5	745	40.1	428	1 EHHU	Ig epsilon chain C
6	741	39.9	426	2 I36948	Ig epsilon chain C
7	587	31.6	572	2 B46529	Ig epsilon chain C
8	560	30.1	504	2 S00390	Ig epsilon chain C
9	499	26.9	627	2 S14683	Ig epsilon chain C
10	490	26.4	479	1 MHRBM	Ig epsilon chain C
11	488.5	26.3	453	2 S37768	Ig epsilon chain C
12	488.5	26.3	474	2 S15590	Ig epsilon chain C
13	488	26.3	458	1 MHRB	Ig epsilon chain C
14	484.5	26.1	391	1 MHHUBT	Ig epsilon chain C
15	477	25.7	452	1 MHHU	Ig epsilon chain C
16	477	25.7	473	1 MHHUM	Ig epsilon chain C
17	469.5	25.3	433	2 S31436	Ig epsilon chain C
18	468	25.2	326	1 MHDG	Ig epsilon chain C
19	464.5	25.0	450	1 MHDG	Ig epsilon chain C
20	464	25.0	328	2 I47161	Ig epsilon chain C
21	461.5	24.8	448	2 S03186	Ig epsilon chain C
22	459.5	24.7	328	2 I47160	Ig epsilon chain C
23	456.5	24.6	328	2 I47159	Ig epsilon chain C
24	455.5	24.5	455	1 MMS	Ig epsilon chain C
25	455.5	24.5	455	2 A24976	Ig epsilon chain C
26	455.5	24.5	476	1 MMSM	Ig epsilon chain C
27	454	24.4	328	2 I47158	Ig epsilon chain C
28	454	24.4	592	2 S25705	Ig epsilon chain C
29	451.5	24.3	327	1 G4HU	Ig epsilon chain C

ALIGNMENTS

RESULT 1
EHRT

Ig epsilon chain C region - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
C:Accession: A93442; A90937; A02143
R:Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6049, 1982
A:Title: Structure and evolution of the heavy chain from rat immunoglobulin E.
A:Reference number: A93442; MUID:83064537; PMID:6292865
A:Accession: A93442
A:Molecule type: mRNA
A:Residues: 1-429 <HEL>
A:Experimental source: strain LOU/c/Wsl, immunocytoma IR2
R:Kinsvoge, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.
DNA 1, 335-343, 1982
A:Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, i
A:Reference number: A90937; MUID:83182019; PMID:6820340
A:Contents: myeloma IR162
A:Accession: A90937
A:Molecule type: mRNA
A:Residues: 'N',169-307,'L',309-342 <KIN>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin C region: immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:19-80/Domain: immunoglobulin homology <IM1>
F:118-186/Domain: immunoglobulin homology <IM2>
F:223-291/Domain: immunoglobulin homology <IM3>
F:327-398/Domain: immunoglobulin homology <IM4>
F:46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predicte

Query Match 56.6%; Score 1051; DB 1; Length 429;
Best Local Similarity 62.6%; Pred. No. 3.7e-70;
Matches 206; Conservative 35; Mismatches 78; Indels 10; Gaps 3;

Qy	17	PVTIIPPTVKLFHSCDPRGDAHSTIQLCLVSGSPAKVHVTVLVDGQEAENLFPYTR	76
Db	97	PVNITKPTVDLLHSCDQNA-FHSTIQYCFYGHQNDVSIHLMDDRKI-----YETH	150
Qy	77	PK-----REGGQTFSLQSEVNITQGMSSNTYTCHVKINGIFEDSSRRCSDEPRGVIT	132
Db	151	AQNVLIKEEGKLASTYSLNITQQMSESTFTCKVQGENYWAHTRCSDDEPRGVIT	210
Qy	133	YLIPSPDLVYENGTPKLTCLVLDSEENITVTWVRERKKSIGSASORSTKHHATTSI	192
Db	211	YLIPSPDLVYENGTPKLTCLVLDSEENITVTWVRERKKSIGSASORSTKHHATTSI	270
Qy	193	TSILPVDADKWIEGEGYQCRVDHHPFKPIVRSITKLPGKRLAPEVYMLPPSPETGTR	252
Db	271	TSILPVDADKWIEGEGYQCRVDHHPFKPIVRSITKAPGKSAPEVYVFLPPEEKKDKR	330

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Qy 253 TVTCLIRGFPSEISVQVLPNNEDHTGHHTTRPKQDGTDPSPFLYSRMLVNSIWEK 312
Db 331 TLTCLIQNFPPEDISVQMLQDSKLPKSOHSTTTPLKNGSNORFIFSRLEVTALWTQ 390
Qy 313 GNLVTRCVVHEALPGSRTRLEKSLHYSAGN 341
Db 391 TKQFTCRVHEALREPRKLERISKSLGN 419

RESULT 2
EHMS
Ig epsilon chain C region (version 1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C:Accession: A02144
R:Li, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.
Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982
A:Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.
A:Reference number: A02144; MUID:83117774; PMID:6818553
A:Accession: A02144
A:Molecule type: mRNA
A:Residues: 1-388 <LIU>
A:Cross-references: GB:J00476; NID:g194875; PIDN:AAA38085.1; PID:g387220
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:11-44/Domain: immunoglobulin homology (fragment) <IM1>
F:81-149/Domain: immunoglobulin homology <IM2>
F:186-254/Domain: immunoglobulin homology <IM3>
F:290-361/Domain: immunoglobulin homology <IM4>
F:10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 50.6%; Score 940.5; DB 1; Length 388;
Best Local Similarity 55.2%; Pred. No. 4.7e-62;
Matches 191; Conservative 46; Mismatches 100; Indels 9; Gaps 5;

Qy 2 FHHHHHTLSLPES-----GPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKV 56
Db 40 FCHVTHPPSFNFESTILVRPNITEPLELHSSCDPNA-FHSTIQLCYCFIYGHILNDV 98
Qy 57 HVTWLVDGQEAENLFPYTRPRREGQTFPSLQSEVNITQGMSSNTYTCVHKHNGSIFE 116
Db 99 SVSWMDDREITDLTAQTVLKEE-GKLASTCSKLNITEQQWSESTFCKTQSGVDYL 157
Qy 117 DSSRCSDDPRGVITYLIPPSPLDLYENGTPKLTCLVLDLSEENITVTVVRERKKSIG 176
Db 158 AHTRPCPDHPRGVITYLIPPSPLDLYQNGAPKLTCLVLDLSEKNVNTWVWQEKTSV- 216
Qy 177 SASQSTKH-HATTSITSLPVDADKWIEGQYQCRVDHPFPKPIVRSITKLPQKRLA 235
Db 217 SASQYTKHNNATTSITSLPVAKDWIEGQYQCRVDHPFPKPIVRSITKLPQKRLA 276
Qy 236 PVMVLPSPPEGTGTRVTCLIRGFPSEISVQVLPNNEDHTGHHTTRPKQDHGTD 295
Db 277 PVYVFPPEESEDKRTLTCLIQNFPPEDISVQMLGDKLINSQHSSTTTLKNGSNQ 336
Qy 296 SPFLYSRMLVNSIWEKGNLVTRCVVHEALPGSRTRLEKSLHYSAGN 341
Db 337 GFFIFSRLEAVTLTQKQFTQCVIHEALQKPRLEKTIISTSLGN 382

RESULT 3
S38864
Ig epsilon chain C region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001
C:Accession: S38864
R:Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A:Description: Combination of a defined specificity and desired isotype by cloning of an
A:Reference number: S38864
A:Accession: S38864
```

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A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-548 <KLP>
A:Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PID:g940782
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:353-421/Domain: immunoglobulin homology <IMM>

Query Match 46.9%; Score 871.5; DB 2; Length 548;
Best Local Similarity 53.9%; Pred. No. 9e-57;
Matches 178; Conservative 45; Mismatches 92; Indels 15; Gaps 5;

Qy 12 LPESGPVTIIPPTVKLFHSSCDPRGD--AHSTIQLCLVSGFSPAKVHTVWLVDGQEAEN 69
Db 229 VPVSSVFIFPPKPK-----DVLTRSTIQLCYCFIYGHILNDVSVSWMDDREITD 278
Qy 70 LFPYTRPRREGQTFPSLQSEVNITQGMSSNTYTCVHKHNGSIFEDSSRRCSDDPRG 129
Db 279 TLAQTVLKEE-GKLASTCSKLNITEQQWSESTFCKTQSGVDYLHTRRCPDHPRG 337
Qy 130 VITVLPSPDLYENGTPKLTCLVLDLSEENITVTVVRERKKSIGSASORSTKH-HA 188
Db 338 VITVLPSPDLYQNGAPKLTCLVLDLSEKNVNTWVWQEKTSV-SASQYTKHNA 396
Qy 189 TTSITSLPVDADKWIEGQYQCRVDHPFPKPIVRSITKLPQKRLADEVVLMPPSPBE 248
Db 397 TTSITSLPVAKDWIEGQYQCRVDHPFPKPIVRSITKLPQKRLADEVVLMPPSPBE 456
Qy 249 GTTRVTCLIRGFPSEISVQVLPNNEDHTGHHTTRPKQDHGTDPSFFLYSRMLVNS 308
Db 457 EDKRTLTCLIQNFPPEDISVQMLGDKLINSQHSSTTTLKNGSNRGGFFIFSRLEV 516
Qy 309 IWEKGNLVTRCVVHEALPGSRTRLEKSLHYS 338
Db 517 LWTQKQFTQCVIHEALQKPRLEKTIIST 546

RESULT 4
EHMS
Ig epsilon chain C region (version 2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996
C:Accession: A02145
R:Ishida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo, T.
EMBO J. 1, 1117-1123, 1982
A:Title: The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison wi
A:Reference number: A90966; MUID:84236092; PMID:6329728
A:Accession: A02145
A:Molecule type: DNA
A:Residues: 1-423 <ISH>
A:Note: the sequence was determined from the germline gene
C:Genetics:
C:Introns: 91/1; 199/1; 307/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:16-77/Domain: immunoglobulin homology <IMM1>
F:115-183/Domain: immunoglobulin homology <IMM2>
F:220-288/Domain: immunoglobulin homology <IMM3>
F:325-396/Domain: immunoglobulin homology <IMM4>
F:23-75,122-181,227-286,332-394/Disulfide bonds: #status predicted
F:43,84,167,239,262,417/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.4%; Score 862.5; DB 1; Length 423;
Best Local Similarity 51.8%; Pred. No. 3e-56;
Matches 183; Conservative 46; Mismatches 103; Indels 21; Gaps 8;

Qy 2 FHHHHHTLSLPESGPVTIIPPTVKLFHS-----SCDPRGDAHSTIQLCLVSGF 51
Db 73 FCHVTHPPSFNFESTILVRPVT---HSLSPPSYSIHRCPDPA-FHSTIQLCYCFIYGH 127
Qy 52 SPKAVHVTWLVDGQEAENLFPYTRPRREGQTFPSLQSEVNITQGMSSNTYTCVHKH 111
```

Db 128 ILNDVSVLWDDREITDTLAQTVLIKSE-GKLASTCSKLNITEQWSESTFTCRVTSQ 186
Qy 112 GSIFEDSSRRCSDDPRGVITYILPPSLDLYENGTPKLTCLVLDSLEENITVTVWRER 171
Db 187 GVDYLAHTRRCRCDHEPRGAITVLIPEPSLDLYQNGAPKLTCLVLDSESEKNVNTWQEK 246
Qy 172 KKSIGSASORSTKHH-HATTSTSTSLPDVADKWIEGEGVQCEVDHPHPKPIVRSITKLP 230
Db 247 KTSV-SASQWYTKHNNATSTSLTPVAKDWIEGYQCVVDPRDPKPIVRSIT-LP 304
Qy 231 --GKLAPEVVMPLSPBETGTRVTCILIRGFYSEISVQWLPNNEDHTGHHTTTRPQ 288
Db 305 QVSQSAEVEVVPPESESEDKRLTCLIQNFPEPDLISQWLGDKLINSQSHTTTP 364
Qy 289 KDHGTRDFFLYSLRMLVKNKSIWEKNLVTCRVVHVALPGSRRTLEKSLHYSAGN 341
Db 365 KNSGNSQGGFFIPSRLEVAKTLWTKQKFTQCVIHEALQKPRKLEKTISTSLGN 417
RESULT 5
EHU
Ig epsilon chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1991 #sequence revision 13-Jun-1993 #text change 16-Jul-1999
C:Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C46
R:Flanagan, J.G.; Rabbits, T.H.
EMBO J. 1, 655-660, 1982
A:Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gene
A:Reference number: A22771; MUID:84236029; PMID:6234164
A:Accession: A22771
A:Molecule type: DNA
A:Residues: 1-428 <FUA>
A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035
R:Ueda, S.; Nakai, S.; Nishida, Y.; Hiseajima, H.; Honjo, T.
EMBO J. 1, 1539-1544, 1982
A:Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudog
A:Reference number: A23195; MUID:84207910; PMID:6327276
A:Accession: A23195
A:Molecule type: DNA
A:Residues: 2-428 <UED>
A:Cross-references: GB:J00222; NID:g184755
R:Zhang, K.; Saxon, A.; Max, E.E.
J. Exp. Med. 176, 233-243, 1992
A:Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing
A:Reference number: PH1214; MUID:92308839; PMID:1613458
A:Accession: PH1214
A:Molecule type: DNA
A:Residues: 320-428 <ZHA>
A:Cross-references: EMBL:X63693; GB:S38668; NID:g32987
R:Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; Sugii
Nucleic Acids Res. 11, 719-726, 1983
A:Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon cha
A:Reference number: A93491; MUID:83168897; PMID:6300763
A:Accession: A93491
A:Molecule type: mRNA
A:Residues: 1-428 <SEN>
A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035
R:Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.
Cell 29, 691-699, 1982
A:Title: Duplication and deletion in the human immunoglobulin epsilon genes.
A:Reference number: A90824; MUID:83001945; PMID:6288268
A:Accession: A90824
A:Molecule type: DNA
A:Residues: 1-358,'L',360-428 <MAX>
A:Cross-references: GB:J00222; NID:g184755
A:Note: this sequence difference may be due to polymorphism
R:Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
A:Reference number: A94418
A:Accession: A94418
A:Molecule type: protein
A:Residues: 'GAWTL',6,'X',8-16,'B',18-43,'B',45-52,55-92,95-97,'B',99-121,'B',123,'L',12
A:Experimental source: myeloma protein Nd

R:Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A:Title: Cloning and sequence determination of the gene for the human immunoglobulin eps
A:Reference number: A93933; MUID:83065234; PMID:6815656
A:Accession: B93933
A:Molecule type: mRNA
A:Residues: 1-40,68-114,427-428 <KEN>
A:Cross-references: GB:L00022; NID:g185035
R:Ikeyama, S.
FEBS Lett. 224, 306-310, 1987
A:Title: Purification and characterization of a recombinant human IgE Fc-epsilon fragmen
A:Reference number: S02438; MUID:88083554; PMID:3121387
A:Accession: S02438
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 98-352 <IKE>
R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
A:Reference number: A53116; MUID:94103254; PMID:8276835
A:Accession: A53116
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 320-428 <ZH>
A:Experimental source: myeloma U266-derived cell line AP-10
A:Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
R:Hellman, L.
Eur. J. Immunol. 23, 159-167, 1993
A:Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of
A:Reference number: A46536; MUID:93122085; PMID:8419166
A:Accession: C46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 382-426 <HEL>
A:Cross-references: GB:S55273; NID:g263166; PIDN:AAB24857.1; PID:g263167
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:125297)
A:Accession: D46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 382-391 <HE2>
A:Cross-references: GB:S55276; NID:g263168; PIDN:AAB24858.1; PID:g263169
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:125299)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AAB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
C:Genetics:
A:Gene: GDB:IGHE
A:Cross-references: GDB:119335; OMIM:147180
A:Map position: 14q32.33-14q32.33
A:Introns: 1/1; 104/1; 211/1; 319/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F:22-87/Domain: immunoglobulin homology <IM1>
F:128-195/Domain: immunoglobulin homology <IM2>
F:232-301/Domain: immunoglobulin homology <IM3>
F:338-407/Domain: immunoglobulin homology <IM4>
F:14/Disulfide bonds: interchain (to light chain) #status predicted
F:15-105,293-85,135-193,239-299,345-405/Disulfide bonds: #status predicted
F:121,49,99,146,252,275/Binding site: carbohydrate (asn) (covalent) #status experimental
F:121,209/Disulfide bonds: interchain (to heavy chain) #status predicted
Query Match 40.1%; Score 745; DB 1; Length 428;
Best Local Similarity 44.4%; Pred. No. 1.5e-47;
Matches 143; Conservative 62; Mismatches 109; Indels 8; Gaps 5;

```
Qy 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVHTWLVQGEAENLFPYVTRPKREG 81
Db 111 PPTVKILQSSCDGGHFPPTIQLCLVSGYTFGTINITWLEDGQVMD--VDLSTASTTQE 168
Qy 82 GQTFSLQSEVNITQGWMSNTYTVCHKHGSIFFEDSSRRCSDDPRGVITYLIPPSPLD 141
Db 169 GELASTQSELTLSQKHLSDRIYTCQVYQGHTFEDSTKCCADSPRGVSAYLSRSPFD 228
Qy 142 LVENGTPKLTCLVLDL-ESEENITVTVWRERKKSIGSASQSRSTKHHATTSTSLPVD 200
Db 229 LPIKSPITITCLVDLAPSKGTWNLTSRASGKPVNHSTRKEKQKRNGLTITVSTLPVGT 288
Qy 201 KDWIEGEGYQCRVDHPHFKPIVRSITKLPGLKLAPEVVMPLPSPRETCG--TRVTCL 258
Db 289 RWIEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAF-ATPEWPSGRDKRTLACLI 347
Qy 259 RGFYSEISVQWLPNNEEDHTGHTTTRPKQDGHGTDPSFFLYSRMLVKNKSIWEKGNLVC 318
Db 348 QNFMPEDISVQWLNHEVQLPDARHSTTQPRKTKGS--GFFVFSRLVTRAWEQKDEFIC 405
Qy 319 RVVHEALPGSRTEKSLHYSAG 340
Db 406 RAVHEAASPSTQVQRAVSNPG 427
RESULT 6
Ig epsilon-chain - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C>Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C:Accession: I36948
R:Sakoyama, Y.; Hong, K.
A:Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orangutan
A:Reference number: I36948; MUID:87147196; PMID:3103123
A:Accession: I36948
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-426 <RES>
A:Cross-references: GB:M15398; NID:g176797; PIDN:AAA35416.1; PID:g176798
A:Introns: 103/1; 209/1; 317/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:336-405/Domain: immunoglobulin homology <IMM>
Query Match 39.9%; Score 741; DB 2; Length 426;
Best Local Similarity 44.5%; Pred. No. 2.9e-47;
Matches 143; Conservative 60; Mismatches 110; Indels 8; Gaps 5;
Qy 23 PTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVHTWLVQGEAENLFPYVTRPKREG 82
Db 110 PTVKVLQSSCDGGHFPPTIQLCLVSGYTFGTINITWLEDGQVMD--VDLSTASTQEG 167
Qy 83 QTFSLQSEVNITQGWMSNTYTVCHKHGSIFFEDSSRRCSDDPRGVITYLIPPSPLD 142
Db 168 ELASTQSELTLSQKHLSDRIYTCQVYQGHTFEDSTKCCADSPRGVSAYLSRSPFDL 227
Qy 143 YENGTPKLTCLVLDL-ESEENITVTVWRERKKSIGSASQSRSTKHHATTSTSLPVD 201
Db 228 FIRKSPITITCLVDLAPSKGTWNLTSRASGKPVNHSTRKEKQKRNGLTITVSTLPVGNR 287
Qy 202 DWIEGEGYQCRVDHPHFKPIVRSITKLPGLKLAPEVVMPLPSPRETCG--TRVTCLIR 259
Db 288 DWIEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAF-ATPEGPGSRDKRTLACLIQ 346
Qy 260 GFVPSISVQWLPNNEEDHTGHTTTRPKQDGHGTDPSFFLYSRMLVKNKSIWEKGNLVC 319
Db 347 NFMPEDISVQWLNHEVQLPDARHSTTQPRKTKGS--GFFVFSRLVTRAWEQKDEFICR 404
Qy 320 VVHEALPGSRTEKSLHYSAG 340
Db 405 AVHEAASPSTQVQRTVSNVNP 425
```

RESULT 7

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Ig Y heavy chain (7.8S) - duck
N:Alternate names: Ig gamma chain (7.8S)
C:Species: Anas platyrhynchos (domestic duck)
C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: B46529; S20759
R:Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J. Immunol. 149, 2627-2633, 1992
A:Title: Structural relationship between the two IGY of the duck, Anas platyrhynchos: mo
A:Reference number: A46529; MUID:93017865; PMID:1401901
A:Accession: B46529
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-572 <MAG>
A:Cross-references: EMBL:X65219; NID:g62442; PIDN:CAA46322.1; PID:g62443
A:Experimental source: spleen
A:Note: sequence extracted from NCBI backbone (NCBIP:116127)
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:37-120/Domain: immunoglobulin homology <IMM>
Query Match 31.6%; Score 587; DB 2; Length 572;
Best Local Similarity 37.3%; Pred. No. 9.8e-36;
Matches 121; Conservative 60; Mismatches 129; Indels 14; Gaps 8;
Qy 22 PPTVKLFHSS-CDPRGDAHSTIQLCLVSGFSPAKVHVHTWLVQGEAENLFPYVTRPKRE 80
Db 249 PPEVQVLHSSVCSLTGDD--DSVELLCVITGFPSPPEVEVEMLVGDGAPA-HLVATMTRPQRE 305
Qy 81 -GGQTFSLQSEVNITQGWMSNTYTVCHKH-NGSIFEDSSRRCSDDPRG--VITYL 134
Db 306 AGSKTYATSTNVSREDWKAGKAFCTCRKHPATGTTAGTGAHARFCPGSGAOSCSPIQIFV 365
Qy 135 IPPSPLDLYENGTPKLTCLVLDLESEENITVTVWRERKKSIGSASQSRSTKHHATTSTITS 194
Db 366 VPPSPGSLYIRQDAKVKHCLVNLPSDASLSISWTRKSGALRPDPMVLTEHFNCTFTASS 425
Qy 195 ILPVDADKDWIEGEGYQCRVDHPHFKPIVRSITKLPGLKLAPEVVMPLPSPRETCGTTTR-T 253
Db 426 SLAISTQDLWAGERFTCTVQHEDLPVPLGKSIAGKAGKVTAPYIFTFFPHAEELSLAEVT 485
Qy 254 VTCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKQDGHGTDPSFFLYSRMLVKNKSIWEKG 313
Db 486 LTCLVRGFPQSEHVEVQWLRNHNVSPPAAEFVTTTPPLKEPNGDGTFFLYSKMTVPVKASWQGG 545
Qy 314 NLATCRVVHEALP--GSRTLEKS 334
Db 546 VSYACVVVHEGLPMRFTORPLOKT 569
RESULT 8
S00390
Ig gamma chain (clone 36) - chicken (fragment)
N:Alternate names: Ig nu chain
C:Species: Gallus gallus (Chicken)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000
C:Accession: S00390
R:Parvari, R.; Avivi, A.; Lentner, F.; Ziv, E.; Tel-Or, S.; Burstein, Y.; Schechter, I.
EMBO J. 7, 739-744, 1988
A:Title: Chicken immunoglobulin gamma-heavy chains: limited VH gene repertoire, combinat
A:Reference number: S00390; MUID:86283642; PMID:3135182
A:Accession: S00390
A:Molecule type: mRNA
A:Residues: 1-504 <PAR>
A:Cross-references: EMBL:X07174
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
Query Match 30.1%; Score 560; DB 2; Length 504;
Best Local Similarity 35.7%; Pred. No. 8.2e-34;
```


Matches 119; Conservative 57; Mismatches 137; Indels 20; Gaps 8;

Qy 17 PVTIIPPTVKLFH-SSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVLDGQEAENLFPYTT 75
Db 172 PVPPVAPEVQVLHASSCTP--SQSEVELLCLVTGFSPASAEVEMLDG--VGGLLVASQ 227

Qy 76 RPKREGGTFSLQSEVNITQGMSSNTYTCHVKH--NGSTFEDSSRRCSD--DEPRGVI 131
Db 228 SPAVRSGSTYSLSSRVNVTGTDWREGKYSRCVRHPATNTVVEDHVKGCPDGAQSCSPIQ 287

Qy 132 TVLIPSPDLIYENGTPKLTCLVLDOSEENITVWWRERKKSIGSASQSRSTKHHHTTS 191
Db 288 LYAIPSPGELYISDAKLRCVLNLPDSSLSVSTWTRKSNLNPDPMPVLQEHFNGTYS 347

Qy 192 ITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPKGLAPEVYMLPPSPBEETGTT 251
Db 348 ASSAVPVSTQDWLSGERFTCTVQHEELPLPSKSVYRNTGPTTPLLIVPFAHPHPELSLS 407

Qy 252 R-TVTCLIRGFYPSISVQWLPNNEEDHTGHTTTRPOKDH-----GTDPSPFLYSRM 303
Db 408 RVTLSCLVRGFRPRDIEIRWLDRHRAVPATEPVTTTAVLPEERTANGAGDGDGDTFFVYSKM 467

Qy 304 LVNKSISWEKGNLVTCTVCRVHVEALP---GSRTEK 333
Db 468 SVETAKWNGTVFACMAVHEALPMRFSORTLOK 500

RESULT 9
S14683
Ig mu chain precursor, membrane-bound (clone 201) - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: S14683; S08047
R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A:Title: Complete nucleoside sequence of the membrane form of the human IGM heavy chain.
A:Reference number: S14683; MUID:90332450; PMID:2115996
A:Accession: S14683
A:Molecule type: mRNA
A:Residues: 1-627 <FRI>
A:Cross-references: EMBL:X17115; NID:g33450; PID:CAA34971.1; PID:g33451
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-627/Product: Ig mu chain #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 26.9%; Score 499; DB 2; Length 627;
Best Local Similarity 31.5%; Pred. No. 3.5e-29;
Matches 106; Conservative 72; Mismatches 135; Indels 24; Gaps 9;

Qy 17 PVTII---PPTVKLFHSSCDPR---GDAHSTIQLCLVSGFSPAKVHVTLVLDGQEAEN 69
Db 284 PLPVIAELPPKVSVP---VPPRDGFEGNPRSKSLICQATGFSPPQIQVSLUREGQVGS 310

Qy 70 LFPYTT-----RPKREGGTFSLQSEVNITQGMSSNTYTCHVKNHSIF-EDSSRRCs 123
Db 311 --GVTTDQVQAEAKESGPTTYKVSTLTILIKESDWLSQSMFTCRVDHRGLTFQGNASSMVCV 368

Qy 124 DDEPRGVITYLIPSPDLIYENGTPKLTCLVLDOSEENITVWWRERKKSIGSASQSRST 183
Db 369 PQDQTAIRVAIPPSFASIFLTKSLTCLVLDLTATYDSVTSWTRQNGEAVKTHTNISE 428

Qy 184 KHHHTTSITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPKRLA-APEVYMLP 242
Db 429 SHPNATPFAVNGEASICEDDWSNGERTCTVTHTDLPSPKQQTISRPKGVALLHRPDPVLLP 488

Qy 243 PSPEETG--TTRTAVTCLIRGFYPSISVQWLPNNEEDHTGHTTTRPOKDHGTDPSPFLY 300
Db 489 PAREQLNRESATITCLVTGFSPADVFVQMQRGQPLSPKEKYTSAPNPEPQAGRYFAH 548

Qy 301 SRMLVNKSIWEKGNLVTCTVCRVHVEALPG---SRTLEKS 334
Db 301 SRMLVNKSIWEKGNLVTCTVCRVHVEALPG---SRTLEKS 334

Db 549 SILTVSEBEWNTGTYTTCVVAHEALPNRVTERTVDKS 585

RESULT 10
MHRBM
Ig mu chain C region, membrane-bound form - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 04-Dec-1986 #sequence_revision 30-Jun-1991 #text_change 23-Aug-1997
C:Accession: A02165; A02164
R:Bernstein, K.E.; Alexander, C.B.; Reddy, E.P.; Mage, R.G.
J. Immunol. 132, 490-495, 1984
A:Title: Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain of V-Ha2 a
A:Reference number: A02164; MUID:84088930; PMID:6418803
A:Contents: a2 allotype
A:Accession: A02165
A:Molecule type: mRNA
A:Residues: 439-479 <BE2>
A:Accession: A02164
A:Molecule type: mRNA
A:Residues: 1-438, 'GRKTYNVSLIMSDTASTCY' <BE3>
C:Note: the sequence of residues 1-438 was assumed to be identical with the corresponding
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F:21-92/Domain: immunoglobulin homology <IMM1>
F:130-202/Domain: immunoglobulin homology <IMM2>
F:242-310/Domain: immunoglobulin homology <IMM3>
F:349-420/Domain: immunoglobulin homology <IMM4>
F:439-479/Domain: carboxyl-terminal <CT8>
F:14/Disulfide bonds: interchain (to light chain) #status predicted
F:28-90,137-200,249-308,356-418/Disulfide bonds: #status predicted
F:46,114,212,261,277,284/Binding site: carbohydrate (Asn) (covalent)
F:219/Disulfide bonds: interchain (to heavy chain) #status predicted
F:296/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted

Query Match 26.4%; Score 490; DB 1; Length 479;
Best Local Similarity 32.4%; Pred. No. 1.1e-28;
Matches 114; Conservative 62; Mismatches 158; Indels 18; Gaps 8;

Qy 5 HHHHTLSLPESGPV-TIIPPTVKLFHSSCDPR-RGDAHSTIQLCLVSGFSPAKVHVTLV 62
Db 94 HSNRNRLRVSPVDSLPNNVSVFIPPRDSFGSGTKRSRLICQATGFSPPQIQSVSMUR 153

Qy 63 DQQAEN---LFPYTTTRPKREGGTFSLQSEVNITQGMSSNTYTCHVKNHSIFEDS- 118
Db 154 DQQVESGVLTKPVEATKGAGPATFSISSMLTITESDWLSQSLYTCRVDRHGFEDKNV 213

Qy 119 --SRRCSDDEPRGVITYLIPSPDLIYENGTPKLTCLVLDOSEENITVWWRERKKSIG 176
Db 214 SMSSECSPTSPGIVQVFPPIAPSFADTFLSKSARLICLVTDLTITYGSLNISWASHNGKALD 273

Qy 177 SASQBSTGHHHTTSITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPKRLA- 235
Db 274 THMNITESHPNATFSAMGEASVCAEDWESGQFTCTVTHTDLPFPPLKHTISK--SREVAK 331

Qy 236 --PEVYMLPPSPES--TGTTRTAVTCLIRGFYPSISVQWLPNNEEDHTGHTTTRPOKDH 291
Db 332 HPPAVYVLPAREQLVRESATVTLVKGFSPADVFVQMQRGQPLSSDKYTSAPAPEP 391

Qy 292 GTDPSFFLYSRMLVNKSIWEKGNLVTCTVCRVHVEALP---GSRTEKSLHYSAG 340
Db 392 QAPGLYFTHSTLTTEEDWNSGETFTCVVCGHEALPHMVTERTVDKSTGEVG 443

RESULT 11
S37768
Ig mu chain C region - human
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 23-Jul-1999
C:Accession: S37768
R:Harindranath, N.; Donadel, G.; Sigounas, G.; Notkins, A.L.
Mol. Immunol. 30, 111-112, 1993

A:Title: Comparison of complete nucleotide sequence of the human IgM heavy chain constant region with the human IgM heavy chain constant region

A:Reference number: S37767; MUID:93109369; PMID:8417370

A:Accession: S37768

A:Molecule type: mRNA

A:Residues: 1-453 <HAR>

A:Cross-references: EMBL:X67301; NID:G38407; PIDN:CAA47714.1; PID:G38408

A:Experimental source: cell line Ab 63

C:Genetics:

A:Map position: 14q32

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: glycoprotein; heterotetramer; immunoglobulin

F:21-90/Domain: immunoglobulin homology <IMM1>

F:127-199/Domain: immunoglobulin homology <IMM2>

F:237-305/Domain: immunoglobulin homology <IMM3>

F:344-415/Domain: immunoglobulin homology <IMM4>

F:14/Disulfide bonds: interchain (to light chain) #status predicted

F:28-88,134-197,244-303,351-413/Disulfide bonds: #status predicted

F:46,209,272,279,440/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:214,452/Disulfide bonds: interchain (to heavy chain) #status predicted

F:291/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted

Query Match 26.3%; Score 488.5; DB 2; Length 453;

Best Local Similarity 31.2%; Pred. No. 1.4e-28;

Matches 105; Conservative 73; Mismatches 134; Indels 25; Gaps 10;

Qy 17 PVTII---PPTVKLFHSSCDPR-----GDAHSTIQLCLVSGFSPAKVHVTVLVDQEAEN 69

Db 102 PLPVIAELPKVSVF---VPRDGFPGNPKS-KLIQATGFSRQIQVSWLRGQVGS 157

Qy 70 LFPYTT-----RPKREGGQTFSLQSEVNITQGMSSNTYTCVHKHNGSIF-EDSSRRCS 123

Db 158 --GVTTDQVQAEKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRLGLTFQONASSMCV 215

Qy 124 DDEPRGVITYLPPSLDLYENGTPKLTCLVLDLESEENITVWVRKKSIGSASQSRST 183

Db 216 PQDQTAIRVFAIPSPASFILTKSTKLTCLVTLDTLTYDSVTISWTRQNGQAVKHTNISE 275

Qy 184 KHHATTSTISILPVDAKDWIEGEGYQCRVDHPHPKPIVRSITKLPKRL-APEVYMLP 242

Db 276 SHPNATFSVAVGEASICEDDMNSGERFTCTVTHTLPSPLKQTIISRPKGVALLHRPDPVYLLP 335

Qy 243 PSPEETG---TTTWTCLIRGFYPSISVQVLPNNEEDHTGHTTTPQKDHGTDPDSFFLY 300

Db 336 PAREQLNLRRESATITCLVTGSPADVFQVMQSGPLSPEKVTISAPMPEQAPGRYFAH 395

Qy 301 SRMLVNSIWKGNLVTCTRVVHEALPG---SRTLEKS 334

Db 396 SILTVSEEMWTGETYTCVVAHEALPNRVTERTVDKS 432

RESULT 12

S15590

Ig heavy chain - human

C:Species: Homo sapiens (man)

C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

C:Accession: S15590

R:Neale, G.A.M.; Kitchingman, G.R.

Nucleic Acids Res. 19, 2427-2433, 1991

A:Title: MRNA transcripts initiating within the human immunoglobulin mu heavy chain enhancer region

A:Reference number: S15590; MUID:91252286; PMID:1904154

A:Accession: S15590

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-474 <NEA>

A:Cross-references: EMBL:X58529

A>Note: the authors translated the codon CAA for residue 265 as Glu

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:344-415/Domain: immunoglobulin homology <IMM>

Query Match 26.3%; Score 488.5; DB 2; Length 474;

Best Local Similarity 31.2%; Pred. No. 1.5e-28;

Matches 105; Conservative 73; Mismatches 134; Indels 25; Gaps 10;

Qy 17 PVTII---PPTVKLFHSSCDPR-----GDAHSTIQLCLVSGFSPAKVHVTVLVDQEAEN 69

Db 102 PLPVIAELPKVSVF---VPRDGFPGNPKS-KLIQATGFSRQIQVSWLRGQVGS 157

Qy 70 LFPYTT-----RPKREGGQTFSLQSEVNITQGMSSNTYTCVHKHNGSIF-EDSSRRCS 123

Db 158 --GVTTDQVQAEKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRLGLTFQONASSMCV 215

Qy 124 DDEPRGVITYLPPSLDLYENGTPKLTCLVLDLESEENITVWVRKKSIGSASQSRST 183

Db 216 PQDQTAIRVFAIPSPASFILTKSTKLTCLVTLDTLTYDSVTISWTRQNGQAVKHTNISE 275

Qy 184 KHHATTSTISILPVDAKDWIEGEGYQCRVDHPHPKPIVRSITKLPKRL-APEVYMLP 242

Db 276 SHPNATFSVAVGEASICEDDMNSGERFTCTVTHTLPSPLKQTIISRPKGVALLHRPDPVYLLP 335

Qy 243 PSPEETG---TTTWTCLIRGFYPSISVQVLPNNEEDHTGHTTTPQKDHGTDPDSFFLY 300

Db 336 PAREQLNLRRESATITCLVTGSPADVFQVMQSGPLSPEKVTISAPMPEQAPGRYFAH 395

Qy 301 SRMLVNSIWKGNLVTCTRVVHEALPG---SRTLEKS 334

Db 396 SILTVSEEMWTGETYTCVVAHEALPNRVTERTVDKS 432

RESULT 12

S15590

Ig heavy chain - human

C:Species: Homo sapiens (man)

C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

C:Accession: S15590

R:Neale, G.A.M.; Kitchingman, G.R.

Nucleic Acids Res. 19, 2427-2433, 1991

A:Title: MRNA transcripts initiating within the human immunoglobulin mu heavy chain enhancer region

A:Reference number: S15590; MUID:91252286; PMID:1904154

A:Accession: S15590

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-474 <NEA>

A:Cross-references: EMBL:X58529

A>Note: the authors translated the codon CAA for residue 265 as Glu

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:344-415/Domain: immunoglobulin homology <IMM>

Query Match 26.3%; Score 488.5; DB 2; Length 474;

Best Local Similarity 31.2%; Pred. No. 1.5e-28;

Matches 105; Conservative 73; Mismatches 134; Indels 25; Gaps 10;

Qy 17 PVTII---PPTVKLFHSSCDPR-----GDAHSTIQLCLVSGFSPAKVHVTVLVDQEAEN 69

Db 102 PLPVIAELPKVSVF---VPRDGFPGNPKS-KLIQATGFSRQIQVSWLRGQVGS 157

Qy 70 LFPYTT-----RPKREGGQTFSLQSEVNITQGMSSNTYTCVHKHNGSIF-EDSSRRCS 123

Db 158 --GVTTDQVQAEKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRLGLTFQONASSMCV 215

Qy 124 DDEPRGVITYLPPSLDLYENGTPKLTCLVLDLESEENITVWVRKKSIGSASQSRST 183

Db 216 PQDQTAIRVFAIPSPASFILTKSTKLTCLVTLDTLTYDSVTISWTRQNGQAVKHTNISE 275

Qy 184 KHHATTSTISILPVDAKDWIEGEGYQCRVDHPHPKPIVRSITKLPKRL-APEVYMLP 242

Db 276 SHPNATFSVAVGEASICEDDMNSGERFTCTVTHTLPSPLKQTIISRPKGVALLHRPDPVYLLP 335

Qy 243 PSPEETG---TTTWTCLIRGFYPSISVQVLPNNEEDHTGHTTTPQKDHGTDPDSFFLY 300

Db 336 PAREQLNLRRESATITCLVTGSPADVFQVMQSGPLSPEKVTISAPMPEQAPGRYFAH 395

Qy 301 SRMLVNSIWKGNLVTCTRVVHEALPG---SRTLEKS 334

Db 396 SILTVSEEMWTGETYTCVVAHEALPNRVTERTVDKS 432

RESULT 12

S15590

Ig heavy chain - human

C:Species: Homo sapiens (man)

C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

C:Accession: S15590

R:Neale, G.A.M.; Kitchingman, G.R.

Nucleic Acids Res. 19, 2427-2433, 1991

A:Title: MRNA transcripts initiating within the human immunoglobulin mu heavy chain enhancer region

A:Reference number: S15590; MUID:91252286; PMID:1904154

A:Accession: S15590

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-474 <NEA>

A:Cross-references: EMBL:X58529

A>Note: the authors translated the codon CAA for residue 265 as Glu

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:344-415/Domain: immunoglobulin homology <IMM>

Query Match 26.3%; Score 488.5; DB 2; Length 474;

Best Local Similarity 31.2%; Pred. No. 1.5e-28;

Matches 105; Conservative 73; Mismatches 134; Indels 25; Gaps 10;

Qy 17 PVTII---PPTVKLFHSSCDPR-----GDAHSTIQLCLVSGFSPAKVHVTVLVDQEAEN 69

Db 102 PLPVIAELPKVSVF---VPRDGFPGNPKS-KLIQATGFSRQIQVSWLRGQVGS 157

Qy 70 LFPYTT-----RPKREGGQTFSLQSEVNITQGMSSNTYTCVHKHNGSIF-EDSSRRCS 123

Db 158 --GVTTDQVQAEKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRLGLTFQONASSMCV 215

Qy 124 DDEPRGVITYLPPSLDLYENGTPKLTCLVLDLESEENITVWVRKKSIGSASQSRST 183

Db 216 PQDQTAIRVFAIPSPASFILTKSTKLTCLVTLDTLTYDSVTISWTRQNGQAVKHTNISE 275

Qy 184 KHHATTSTISILPVDAKDWIEGEGYQCRVDHPHPKPIVRSITKLPKRL-APEVYMLP 242

Db 276 SHPNATFSVAVGEASICEDDMNSGERFTCTVTHTLPSPLKQTIISRPKGVALLHRPDPVYLLP 335

Qy 243 PSPEETG---TTTWTCLIRGFYPSISVQVLPNNEEDHTGHTTTPQKDHGTDPDSFFLY 300

Db 336 PAREQLNLRRESATITCLVTGSPADVFQVMQSGPLSPEKVTISAPMPEQAPGRYFAH 395

Qy 301 SRMLVNSIWKGNLVTCTRVVHEALPG---SRTLEKS 334

Db 396 SILTVSEEMWTGETYTCVVAHEALPNRVTERTVDKS 432

RESULT 12

S15590

Ig heavy chain - human

C:Species: Homo sapiens (man)

C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

C:Accession: S15590

R:Neale, G.A.M.; Kitchingman, G.R.

Nucleic Acids Res. 19, 2427-2433, 1991

A:Title: MRNA transcripts initiating within the human immunoglobulin mu heavy chain enhancer region

A:Reference number: S15590; MUID:91252286; PMID:1904154

A:Accession: S15590

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-474 <NEA>

A:Cross-references: EMBL:X58529

A>Note: the authors translated the codon CAA for residue 265 as Glu

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:344-415/Domain: immunoglobulin homology <IMM>

Query Match 26.3%; Score 488.5; DB 2; Length 474;

Best Local Similarity 31.2%; Pred. No. 1.5e-28;

Matches 105; Conservative 73; Mismatches 134; Indels 25; Gaps 10;

Qy 17 PVTII---PPTVKLFHSSCDPR-----GDAHSTIQLCLVSGFSPAKVHVTVLVDQEAEN 69

Db 102 PLPVIAELPKVSVF---VPRDGFPGNPKS-KLIQATGFSRQIQVSWLRGQVGS 157

Qy 70 LFPYTT-----RPKREGGQTFSLQSEVNITQGMSSNTYTCVHKHNGSIF-EDSSRRCS 123

Db 158 --GVTTDQVQAEKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRLGLTFQONASSMCV 215

Qy 124 DDEPRGVITYLPPSLDLYENGTPKLTCLVLDLESEENITVWVRKKSIGSASQSRST 183

Db 216 PQDQTAIRVFAIPSPASFILTKSTKLTCLVTLDTLTYDSVTISWTRQNGQAVKHTNISE 275

Qy 184 KHHATTSTISILPVDAKDWIEGEGYQCRVDHPHPKPIVRSITKLPKRL-APEVYMLP 242

Db 276 SHPNATFSVAVGEASICEDDMNSGERFTCTVTHTLPSPLKQTIISRPKGVALLHRPDPVYLLP 335

Qy 243 PSPEETG---TTTWTCLIRGFYPSISVQVLPNNEEDHTGHTTTPQKDHGTDPDSFFLY 300

Db 336 PAREQLNLRRESATITCLVTGSPADVFQVMQSGPLSPEKVTISAPMPEQAPGRYFAH 395

Qy 301 SRMLVNSIWKGNLVTCTRVVHEALPG---SRTLEKS 334

Db 396 SILTVSEEMWTGETYTCVVAHEALPNRVTERTVDKS 432

RESULT 12

S15590

Ig heavy chain - human

C:Species: Homo sapiens (man)

C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

C:Accession: S15590

R:Neale, G.A.M.; Kitchingman, G.R.

Nucleic Acids Res. 19, 2427-2433, 1991

A:Title: MRNA transcripts initiating within the human immunoglobulin mu heavy chain enhancer region

A:Reference number: S15590; MUID:91252286; PMID:1904154

A:Accession: S15590

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-474 <NEA>

A:Cross-references: EMBL:X58529

A>Note: the authors translated the codon CAA for residue 265 as Glu

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:344-415/Domain: immunoglobulin homology <IMM>

Query Match 26.3%; Score 488.5; DB 2; Length 474;

Best Local Similarity 31.2%; Pred. No. 1.5e-28;

Matches 105; Conservative 73; Mismatches 134; Indels 25; Gaps 10;

Qy 17 PVTII---PPTVKLFHSSCDPR-----GDAHSTIQLCLVSGFSPAKVHVTVLVDQEAEN 69

Db 102 PLPVIAELPKVSVF---VPRDGFPGNPKS-KLIQATGFSRQIQVSWLRGQVGS 157

Qy 70 LFPYTT-----RPKREGGQTFSLQSEVNITQGMSSNTYTCVHKHNGSIF-EDSSRRCS 123

Db 158 --GVTTDQVQAEKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRLGLTFQONASSMCV 215

Qy 124 DDEPRGVITYLPPSLDLYENGTPKLTCLVLDLESEENITVWVRKKSIGSASQSRST 183

Db 216 PQDQTAIRVFAIPSPASFILTKSTKLTCLVTLDTLTYDSVTISWTRQNGQAVKHTNISE 275

Qy 184 KHHATTSTISILPVDAKDWIEGEGYQCRVDHPHPKPIVRSITKLPKRL-APEVYMLP 242

Db 276 SHPNATFSVAVGEASICEDDMNSGERFTCTVTHTLPSPLKQTIISRPKGVALLHRPDPVYLLP 335

Qy 243 PSPEETG---TTTWTCLIRGFYPSISVQVLPNNEEDHTGHTTTPQKDHGTDPDSFFLY 300

Db 336 PAREQLNLRRESATITCLVTGSPADVFQVMQSGPLSPEKVTISAPMPEQAPGRYFAH 395

Qy 301 SRMLVNSIWKGNLVTCTRVVHEALPG---SRTLEKS 334

Db 396 SILTVSEEMWTGETYTCVVAHEALPNRVTERTVDKS 432

RESULT 12

S15590

Ig heavy chain - human

C:Species: Homo sapiens (man)

C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

Db 162 TREGNVT-STHSELNITQGEWTSQKTYTTCQVYQGFDFDEARKCESDPRGVTSYLSPP 220
Qy 138 SPLDLYENGTPKLTCLVLDLESEENITVTVWRERKKSIGSASQSTKHHATTSTISILP 197
Db 221 SPLDLYVHKAPKITCLVLDLATMEGMNLTWYRESKEPVNPGPLNKKDHFNGTITVTSTLP 280
Qy 198 VDAKWIEGEGYQCRVDHHPFKPIVRSITKLPKGLAPENVMLPPSPRETGTTR--TVT 255
Db 281 VNTNDWIEGETYTCRVTHPHLPKDIVRSIAKAPGRAPDPVYFLFPPPEEQTKDRVLT 340
Qy 198 VDAKWIEGEGYQCRVDHHPFKPIVRSITKLPKGLAPENVMLPPSPRETGTTR--TVT 255
Db 281 VNTNDWIEGETYTCRVTHPHLPKDIVRSIAKAPGRAPDPVYFLFPPPEEQTKDRVLT 340
Qy 256 CLIRGFYPSSEISVQWLNNEDHTGHTTTRPKQDHGTDPSPFSLYRMLVNKSIWEKGNL 315
Db 341 CLIQNFFPADISVQWLNRNDSPITQDYTTTGHKVGSGRPAPFIFSRLEVSRVDWEQKNK 400
Qy 316 VTCRVVHEALPGSRTLEKSLHYSAG 340
Db 401 FTCQVVHEALSGSRILOKXVSKTPG 425
RESULT 2
PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-13795-2
Query Match 51.2%; Score 950.5; DB 5; Length 426;
Best Local Similarity 53.8%; Pred. No. 2.2e-86;
Matches 175; Conservative 52; Mismatches 95; Indels 3; Gaps 2;
Qy 18 VTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSAPKVVHVTWLDQGBAENLFPYVTPRP 77
Db 102 LNFIPPTVKLFHSSCNPNVGDTHTIQLLCLISGYVPGDMEVILWLDQKATNIFPYTAPG 161
Qy 78 KREGGQTFSLQSEVNITQCGWSSNTYTCVHKINGSIFEDSSRRCSDDPRGVITYLIPP 137
Db 162 TREGNVT-STHSELNITQGEWTSQKTYTTCQVYQGFDFDEARKCESDPRGVTSYLSPP 220
Qy 138 SPLDLYENGTPKLTCLVLDLESEENITVTVWRERKKSIGSASQSTKHHATTSTISILP 197

Db 221 SPLDLYVHKAPKITCLVLDLATMEGMNLTWYRESKEPVNPGPLNKKDHFNGTITVTSTLP 280
Qy 198 VDAKWIEGEGYQCRVDHHPFKPIVRSITKLPKGLAPENVMLPPSPRETGTTR--TVT 255
Db 281 VNTNDWIEGETYTCRVTHPHLPKDIVRSIAKAPGRAPDPVYFLFPPPEEQTKDRVLT 340
Qy 256 CLIRGFYPSSEISVQWLNNEDHTGHTTTRPKQDHGTDPSPFSLYRMLVNKSIWEKGNL 315
Db 341 CLIQNFFPADISVQWLNRNDSPITQDYTTTGHKVGSGRPAPFIFSRLEVSRVDWEQKNK 400
Qy 316 VTCRVVHEALPGSRTLEKSLHYSAG 340
Db 401 FTCQVVHEALSGSRILOKXVSKTPG 425
RESULT 3
US-09-192-545-2
; Sequence 2, Application US/09192545
; Patent No. 6118044
; GENERAL INFORMATION:
; APPLICANT: Karasuyama, Hajime
; APPLICANT: Yonekawa, Hiromichi
; APPLICANT: Taya, Choji
; APPLICANT: Matsuo, Kunie
; TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
; FILE REFERENCE: 799P79570
; CURRENT APPLICATION NUMBER: US/09/192,545
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: JP HEI 9-313989
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: Designed heavy
US-09-192-545-2
Query Match 46.4%; Score 862.5; DB 3; Length 561;
Best Local Similarity 51.8%; Pred. No. 1.9e-77;
Matches 183; Conservative 46; Mismatches 103; Indels 21; Gaps 8;
Qy 2 FHHHHHTLSLPESGPVTIIPPTVKLFHS-----SCDPRGDAHSTIQLLCLVSGF 51
Db 211 FTCVHTPPSPFNSERTILVREPT---HSLSPWPWSYSHRCDPNA-PHSTIQLYCFIYGH 265
Qy 52 SPAKVHTWLDVQGBAENLFPYVTPRKREGGQTFSLQSEVNITQCGWSSNTYTCVHKXN 111
Db 266 ILNDVSVWLMDREITDTLAQTVLKEE-GKLASTCCKLNITEQOWMSESTFCRVTSQ 324
Qy 112 GSIFEDSSRRCSDDPRGVITYLIPPSPLDLYENGTPKLTCLVLDLESEENITVTVWRER 171
Db 325 GVDYLAHTRRCPDHEPGAITVLIIPPSPLDLYQNGAPKLTCLVLDLESEKKNVNTWNOEK 384
Qy 172 KKSIGSASQSTKHH-HATTSTISILPVDADKWIEGEGYQCRVDHHPFKPIVRSITKLP 230
Db 385 KTSV-SASQWYTKHHNATTSITSLPVVAKDWIEGEGYQCVVDRPDPFKPIVRSIT-LP 442
Qy 231 --GKLAPEVYMLPPSPRETGTTRVTCLIRGFYPSSEISVQWLNNEDHTGHTTTRPQ 288
Db 443 QVSQSAPEVYVFPPEPESEDKRTLTCLIQNFFPEDISVQWLGDGKLSINSHQSTTTPL 502
Qy 289 KDHGTDPSFFLYRMLVNKSIWEKGNLTVTCRVVHEALPGSRTLEKSLHYSAGN 341
Db 503 KNSGNSQGGFFIFSRLEVAKLTWTKQKQTCQVIEALQKPKLEKTIISTISLGN 555
RESULT 4
US-08-646-981-17
; Sequence 17, Application US/08646981
; Patent No. 5852183

```

; GENERAL INFORMATION:
; APPLICANT: MAEDA, HIROAKI
; APPLICANT: EDA, YASUYUKI
; APPLICANT: KIMACHI, KAZUHIKO
; APPLICANT: KIMACHI, KAZUHIKO
; APPLICANT: ONO, YOICHI
; APPLICANT: TOKIYOSHI, SACHIO
; TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE
; TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
; TITLE OF INVENTION: IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,981
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1488-106
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-646-981-17

Query Match 27.3%; Score 507; DB 2; Length 331;
Best Local Similarity 35.2%; Pred. No. 2.3e-42;
Matches 118; Conservative 69; Mismatches 122; Indels 26; Gaps 11;

Qy 23 PTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVVDGQEAENLFPYTTTPKREG 82
Db 5 PSVPFLAPSCG--STSGSTVTLACLIVSGYFPEPVTWSV--NSGSLTSGVHTTTPSVLKSSG- 60

Qy 83 QTFSLQSEVNITQGWMSNTYTCVKNKS-----IFEDSSRRCSDDPE-----RG 129
Db 61 -LYSLSSMTVPSSR-LPSETFTCNVHVHPATNTKVDKPGVPKESCKGICSPCPVESLGG 118

Qy 130 VITYLIPPSPLDYE-NCTPKLTCLVLDLESEE-NITVTWVRERKKSIGSASQSRSTKHH 187
Db 119 PSVFIFPPFKDILRITPEVTCVVDLGRDPEVQISWFVDGKEVHTAKTPREQQFN 178

Qy 188 ATTSITSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPVYMLPPSP 247
Db 179 STYRVSVLPVIEHQDLATGKEFKCRVNHGLSPPIERTISKARGQAHQPGVTVLPSPKE 238

Qy 248 --TGTTRVTCLIRGFYSEISVQMLPNNEDHTGHTTTTPQKHGDTDPFFLYSRMLV 305
Db 239 LSSSDTVTLTCLIKDFPPFIDVEMQSQGQPEPESKYHTTAPQLDE--DGSYFLYSLSV 296

Qy 306 NKSIWEKNLTCRVVHEALPGSRRTLEKSLHYSAG 340
Db 297 DKSRWEQGDPTTCVAVHEALQNHYT-DLSLSHSPG 330

RESULT 5
US-08-646-981-16
; Sequence 16, Application US/08646981
; Patent No. 5852183
; GENERAL INFORMATION:
; APPLICANT: Soulliou, Jean-Paul

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; APPLICANT: MAEDA, HIROAKI
; APPLICANT: EDA, YASUYUKI
; APPLICANT: KIMACHI, KAZUHIKO
; APPLICANT: KIMACHI, KAZUHIKO
; APPLICANT: ONO, YOICHI
; APPLICANT: TOKIYOSHI, SACHIO
; TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE
; TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
; TITLE OF INVENTION: IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,981
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1488-106
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-646-981-16

Query Match 26.6%; Score 493.5; DB 2; Length 334;
Best Local Similarity 33.9%; Pred. No. 5.3e-41;
Matches 116; Conservative 68; Mismatches 121; Indels 37; Gaps 11;

Qy 23 PTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV-----LVDGQEAENLFPYTTTPK 78
Db 5 PSVPFLAPSCG--STSGSTVALACLIVSGYFPEPVTWSVNSGSLTSG-----VHTFSD 55

Qy 79 REGQTSLOSEVNITQGWMSNTYTCVKNKS---IFEDSSRRCSDDPE----- 128
Db 56 LQSSGLYSLSSMTVPSSRW--SSETFTCNVHVHPATNTKVDKPGVPKREGRVPRPPDCPKC 114

Qy 129 -----GVITYLIPPSPLD-LYENGTPKLTCLVLDLESEE-NITVTWVRERKKSIGSAS 179
Db 115 PAPMLGSPSVFIPEPKPKDTLLIARTPEVTCVVDLGPEDPEVQISWFDGKQMTAKT 174

Qy 180 QRSTKHHHTTSTSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPVY 239
Db 175 QPREQFNGTVRVVSVLPVIGHQDLKKGQFTCKVNNKALPSPIERTISKARGQAHQPSVY 234

Qy 240 MLPPSPPE--TGTTRVTCLIRGFYSEISVQMLPNNEDHTGHTTTTPQKHGDTDPFF 298
Db 235 VLPPSRELSNTVSLTCLIKDFPPFIDVEMQSQGQPEPESKYRTTTPQLDE--DGSYF 292

Qy 299 LYSRLVKNKSIWEKNLTCRVVHEALPGSRRTLEKSLHYSAG 340
Db 293 LYSKLSVDKSRWQGDPTTCVAVHEALQNHYT-QKSLSHSPG 333

RESULT 6
US-07-932-915-2
; Sequence 2, Application US/07932915
; Patent No. 5672486
; GENERAL INFORMATION:
; APPLICANT: Soulliou, Jean-Paul

```

;; TITLE OF INVENTION: Protein Polyligands Joined To A Stable Protein
;; TITLE OF INVENTION: Core
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
;; STREET: 5 Palo Alto Square, Suite 400
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94306
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/932,915
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/646,875
;; FILING DATE: 28-JAN-1991
;; APPLICATION NUMBER: US 07/575,394
;; FILING DATE: 23-AUG-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rowland Ph.D., Bertram I.
;; REGISTRATION NUMBER: 20,015
;; REFERENCE/DOCKET NUMBER: ATLA-001/0105
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-494-7622
;; TELEFAX: 415-857-0663
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 504 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-07-932-915-2

Query Match 26.3%; Score 488; DB 1; Length 504;
Best Local Similarity 31.2%; Pred. No. 3.5e-40;
Matches 103; Conservative 72; Mismatches 133; Indels 22; Gaps 9;
Qy 21 IPPTVKLFHSSCDPR----GDAHSTIQLCLVSGSPAKVHVTVLWDGQAEENLPFYTT- 75
Db 160 LPPKVSFV---VPRDGFNGPRKS-KLICQATGSPQIQVSWLRGKQVGS--GVTTD 213
Qy 76 ----RPKREGGQTSLSQSEVNITQGMSSNTYTVCHVKGHSIF-EDSSRRCSDDPRGV 130
Db 214 QVQAEAKESGPTYKYVTSITLIKESDWLSQSMFTCEVDHRLGTLFQNASMCMVDPDQTAI 273
Qy 131 IYLIPLPSPLDYENGTPKLTCLVLDLSEENITVTVWRERKKSIGSASQSTKHHHTT 190
Db 274 RVFAIPPSFASIFLTKSTKLTLVDTLTYDSVTISWTRQNGEAVKTHNISHPNATF 333
Qy 191 SITSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGKRL-APEVYMLPPSPPEETG 249
Db 334 SAVGEASICEDDWSNGERFTCTVTHDPLSPKQIISRPGKVALHRPDVYLLPPAREQLN 393
Qy 250 --TTRVTCLIRGFVPSISVQWLPNNEDHTGHHTTRPKDHDGTDPSFFLYSRMLVNK 307
Db 394 LRESATITCLTVGFSPADVFVQWQMGQPLSPKQIISRPGKVALHRPDVYLLPPAREQLN 393
Qy 308 SIWEKGNLVTCRVVHEALPG---SRTLEKS 334
Db 454 EEWNTGETYTCVVAHEALPNRVRTVDKS 483

RESULT 7

PCT-US91-05826-2
; Sequence 2, Application PC/TUS9105826
; GENERAL INFORMATION:
; APPLICANT: Soullillon, Jean-Paul

;; TITLE OF INVENTION: Protein Polyligands Joined To A Stable Protein
;; TITLE OF INVENTION: Core
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Bertram I. Rowland, Ph.D.
;; STREET: 4 Embarcadero Center, Suite 3400
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US91/05826
;; FILING DATE: 19910822
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/575,394
;; FILING DATE: 29-AUG-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rowland Ph.D., Bertram I.
;; REGISTRATION NUMBER: 20,015
;; REFERENCE/DOCKET NUMBER: PP55352-1/BIR
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-494-8771
;; TELEFAX: 415-494-8771
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 504 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US91-05826-2

Query Match 26.3%; Score 488; DB 5; Length 504;
Best Local Similarity 31.2%; Pred. No. 3.5e-40;
Matches 103; Conservative 72; Mismatches 133; Indels 22; Gaps 9;
Qy 21 IPPTVKLFHSSCDPR----GDAHSTIQLCLVSGSPAKVHVTVLWDGQAEENLPFYTT- 75
Db 160 LPPKVSFV---VPRDGFNGPRKS-KLICQATGSPQIQVSWLRGKQVGS--GVTTD 213
Qy 76 ----RPKREGGQTSLSQSEVNITQGMSSNTYTVCHVKGHSIF-EDSSRRCSDDPRGV 130
Db 214 QVQAEAKESGPTYKYVTSITLIKESDWLSQSMFTCEVDHRLGTLFQNASMCMVDPDQTAI 273
Qy 131 IYLIPLPSPLDYENGTPKLTCLVLDLSEENITVTVWRERKKSIGSASQSTKHHHTT 190
Db 274 RVFAIPPSFASIFLTKSTKLTLVDTLTYDSVTISWTRQNGEAVKTHNISHPNATF 333
Qy 191 SITSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGKRL-APEVYMLPPSPPEETG 249
Db 334 SAVGEASICEDDWSNGERFTCTVTHDPLSPKQIISRPGKVALHRPDVYLLPPAREQLN 393
Qy 250 --TTRVTCLIRGFVPSISVQWLPNNEDHTGHHTTRPKDHDGTDPSFFLYSRMLVNK 307
Db 394 LRESATITCLTVGFSPADVFVQWQMGQPLSPKQIISRPGKVALHRPDVYLLPPAREQLN 393
Qy 308 SIWEKGNLVTCRVVHEALPG---SRTLEKS 334
Db 454 EEWNTGETYTCVVAHEALPNRVRTVDKS 483

RESULT 8

US-08-436-463-6
; Sequence 6, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki

APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI=1
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-463-6

Query Match 25.6%; Score 475.5; DB 1; Length 333;
Best Local Similarity 32.7%; Pred. No. 3.3e-39;
Matches 112; Conservative 72; Mismatches 121; Indels 37; Gaps 12;

Qy 23 PTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW----LVDGQBAENLFPYVTRPK 78
Db 4 PSVFPPLAPSCGTGSGA--TVALACLVLGYFPPEVTVSMNSGALTSG---VHTFPAVL--- 55

Qy 79 REGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFE--DSRRCSDDP----- 127
Db 56 -QASGLYSLSMVTVPSRWL--SDTFTCNVAHPSPNTKVKDTRKTDHPGPKPCDCPKC 113

Qy 128 -----RGVITVLIAPPSPLD--LYENGTPKLTCLVLDL--ESENITVTVWRERKKSIGSAS 179
Db 114 PPPEMLGSPSIFIPPKPKDILSRTEVTVCLVLDLPDSDVQITWFDVNTQVYVTAKT 173

Qy 180 QRSTKHHHTTSITSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPKRLAPEVY 239
Db 174 SPREEQFNSTVRVSVLPILHQDLKGEKFKVNSKSLPSPIERTISKAKQPHEPVY 233

Qy 240 MLPSPSETGTTR--TVTCLIRGFYPSSEISVQWLPNNEEDHTGHHTTTPKQDHGTDPSFF 298
Db 234 VLPPAQEELSRNKVSVTCLIKSFHPDIAVEWITGOPEPENNYRTTTPOLD--SDGTIF 291

Qy 299 LYSRLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAG 340
Db 292 VYSLVDRSHWQRGNVTYTCVSHEALSHHT--QKSLTQSPG 332

RESULT 9
US-08-024-253-6
Sequence 6, Application US/08024253
Patent No. 5785968
GENERAL INFORMATION:

APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
APPLICANT: TOHYA, Yukinobu
APPLICANT: MIKAMI, Takeehi
TITLE OF INVENTION: ANTI-FELINE CALCIVIRUS RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT ENCODING THE SAME
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER
STREET: 1233 20th Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-8218
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/024,253
FILING DATE: 19930301
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 79189/1992
FILING DATE: 28-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: CANTOR, Herbert I.
REGISTRATION NUMBER: 24,392
REFERENCE/DOCKET NUMBER: P-500-23744
TELEPHONE: (202) 887-0400
TELEFAX: (202) 835-0605
TELEX: 440706 WEGBR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-024-253-6

Query Match 25.6%; Score 475.5; DB 1; Length 333;
Best Local Similarity 32.7%; Pred. No. 3.3e-39;
Matches 112; Conservative 72; Mismatches 121; Indels 37; Gaps 12;

Qy 23 PTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW----LVDGQBAENLFPYVTRPK 78
Db 4 PSVFPPLAPSCGTGSGA--TVALACLVLGYFPPEVTVSMNSGALTSG---VHTFPAVL--- 55

Qy 79 REGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFE--DSRRCSDDP----- 127
Db 56 -QASGLYSLSMVTVPSRWL--SDTFTCNVAHPSPNTKVKDTRKTDHPGPKPCDCPKC 113

Qy 128 -----RGVITVLIAPPSPLD--LYENGTPKLTCLVLDL--ESENITVTVWRERKKSIGSAS 179
Db 114 PPPEMLGSPSIFIPPKPKDILSRTEVTVCLVLDLPDSDVQITWFDVNTQVYVTAKT 173

Qy 180 QRSTKHHHTTSITSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPKRLAPEVY 239
Db 174 SPREEQFNSTVRVSVLPILHQDLKGEKFKVNSKSLPSPIERTISKAKQPHEPVY 233

Qy 240 MLPSPSETGTTR--TVTCLIRGFYPSSEISVQWLPNNEEDHTGHHTTTPKQDHGTDPSFF 298
Db 234 VLPPAQEELSRNKVSVTCLIKSFHPDIAVEWITGOPEPENNYRTTTPOLD--SDGTIF 291

Qy 299 LYSRLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAG 340
Db 292 VYSLVDRSHWQRGNVTYTCVSHEALSHHT--QKSLTQSPG 332

RESULT 10
US-08-788-800-12
; Sequence 12, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Correll E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-788-800-12

Query Match 25.6%; Score 475; DB 2; Length 450;
Best Local Similarity 34.7%; Pred No. 5.8e-39;
Matches 112; Conservative 66; Mismatches 115; Indels 30; Gaps 12;
Qy 35 RGDASTIQLLCLVSGFSPAKVHVTVW----LVDGQEAENLFPYTRPKREGGQTFSLQSE 90
Db 140 RSTSESTAALGCLVKDYFPEPTVSNWNSGALTSG---VHTFPAVL---QSSGLYSLSSV 192
Qy 91 VNITQGMSSNTYTCVHKH---NGSIFEDSSRRCSDDDEP-----RGVITYLIPPSPL 140
Db 193 VVTSSNF-GTQTYTCNVDPKPSNTKVDKTVKRCVCCPCPPAPPVAGPSVFLFPKPK 251
Qy 141 D-LYENGTPKLTCLVLDLESEE-NITVTWVERKKSIGASQSTKHHHATTSITSLPV 198
Db 252 DTLMISRTPEVTCVVDVSHEDPEQFNWYDGMVHNKAKTPREEQFNSTFRVSVLTV 311
Qy 199 DAKWIEGEGYQCRVDHPHFKPIVRSITKLPKGLAPEVYMLPPSPPEE-TGTTTRVTCL 257
Db 312 VHODMLNGKEYCKVSNKGLPAPIEKTISKTKGQPREQVYTLPPSREEMTKNQVSLTCL 371
Qy 258 IRGFYPSISVQWLPNNEEDHTGHTTTPQKDHGTDSPFFLYSRMLVKNYSIWEKGNLTV 317
Db 372 VRGFYPSDIAVWESNGQPEN--NYKTTTPMLD--SDGSFFLYSKLTVDKSRWQGNVFS 427
Qy 318 CRVVEALPGSRITLKSILHSYAG 340
Db 428 CSVMHEALHNHYT-QKSLSLSPG 449

RESULT 11
US-07-934-373C-23
; Sequence 23, Application US/07934373C

; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-23

Query Match 25.6%; Score 475; DB 2; Length 469;
Best Local Similarity 34.7%; Pred No. 6.2e-39;
Matches 112; Conservative 66; Mismatches 115; Indels 30; Gaps 12;
Qy 35 RGDASTIQLLCLVSGFSPAKVHVTVW----LVDGQEAENLFPYTRPKREGGQTFSLQSE 90
Db 159 RSTSESTAALGCLVKDYFPEPTVSNWNSGALTSG---VHTFPAVL---QSSGLYSLSSV 211
Qy 91 VNITQGMSSNTYTCVHKH---NGSIFEDSSRRCSDDDEP-----RGVITYLIPPSPL 140
Db 212 VVTSSNF-GTQTYTCNVDPKPSNTKVDKTVKRCVCCPCPPAPPVAGPSVFLFPKPK 270
Qy 141 D-LYENGTPKLTCLVLDLESEE-NITVTWVERKKSIGASQSTKHHHATTSITSLPV 198
Db 271 DTLMISRTPEVTCVVDVSHEDPEQFNWYDGMVHNKAKTPREEQFNSTFRVSVLTV 330
Qy 199 DAKWIEGEGYQCRVDHPHFKPIVRSITKLPKGLAPEVYMLPPSPPEE-TGTTTRVTCL 257
Db 331 VHODMLNGKEYCKVSNKGLPAPIEKTISKTKGQPREQVYTLPPSREEMTKNQVSLTCL 390
Qy 258 IRGFYPSISVQWLPNNEEDHTGHTTTPQKDHGTDSPFFLYSRMLVKNYSIWEKGNLTV 317
Db 391 VRGFYPSDIAVWESNGQPEN--NYKTTTPMLD--SDGSFFLYSKLTVDKSRWQGNVFS 446
Qy 318 CRVVEALPGSRITLKSILHSYAG 340
Db 447 CSVMHEALHNHYT-QKSLSLSPG 468

RESULT 12
US-08-437-642B-23

Sequence 23, Application US/08437642B
 Patent No. 6054297
 GENERAL INFORMATION:
 APPLICANT: Paul J. Carter
 APPLICANT: Leonard G. Presta
 TITLE OF INVENTION: Immunoglobulin Variants
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/437,642B
 FILING DATE: 09-May-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/934373
 FILING DATE: 21-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/146206
 FILING DATE: 17-NOV-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/05126
 FILING DATE: 15-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0709P2C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 469 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-437-642B-23

Query Match 25.6%; Score 475; DB 3; Length 469;
 Best Local Similarity 34.7%; Pred. No. 6.2e-39;
 Matches 112; Conservative 66; Mismatches 115; Indels 30; Gaps 12;

Qy 35 RGDASTIQLCLVSGFSPAKVHVW----LVDGQEAENLPYTRPRKREGQTSLOSE 90
 Db 159 RSTSESTAALGLKVDYFPEPVTVSWNSGALTSG---VHTPPAVL-----QSSGLYSLSSV 211
 Qy 91 VNITQGMSSNTYTCVHKH---NGSIFEDSSRRCSDDP-----RGVITYLIPPSPL 140
 Db 212 VVTSSNP-GTQTYTCNVDRKPSNTKVDKTVKCKVCCPCPAPVAGPSVFLFPKPK 270
 Qy 141 D-LYENGTPKLTCLVLDLESEE-NITVTWVRERKKSIGASQSTKHHHATTSITSLPV 198
 Db 271 DTLMSRTPETVTCVVVDVSHEDPEVFQFNWYDGMVHNAKTPREEQFNSTFRVVSULTV 330
 Qy 199 DAKDWIEGEGQCRVDHPFPKPIVRSITKLPGKRLAPEVYMLPPSPPE-TGTTTRVTCL 257
 Db 331 VHQDWLNGKEYCKKSNKGLPAPIETKISKTKGQPREQVYTLPPSREEMTKNQVSLTCL 390
 Qy 258 IRGFYPSISVQWLPNNEDHTGHTHTTRPQKDHGTDPSFFLYSRMLVKNKSIWEKGNLVT 317
 Db 391 VKGFYPSIDIAWESNGQPEN--NYKTTTPMLD--SDGSFFLYSKLTVDKSRWQQGNVFS 446

Qy 318 CRVVEALPGSRITLEKSLHYSAG 340
 Db 447 CSVMHEALHNHYT-QKSLSLSPG 468

RESULT 13
 US-08-146-206C-23
 Sequence 23, Application US/08146206C
 Patent No. 6407213
 GENERAL INFORMATION:
 APPLICANT: Carter, Paul J.
 APPLICANT: Presta, Leonard G.
 TITLE OF INVENTION: Method For Making Humanized Antibodies
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/146,206C
 FILING DATE: 17-No. 6407213-1993
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0709P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 469 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-146-206C-23

Query Match 25.6%; Score 475; DB 4; Length 469;
 Best Local Similarity 34.7%; Pred. No. 6.2e-39;
 Matches 112; Conservative 66; Mismatches 115; Indels 30; Gaps 12;

Qy 35 RGDASTIQLCLVSGFSPAKVHVW----LVDGQEAENLPYTRPRKREGQTSLOSE 90
 Db 159 RSTSESTAALGLKVDYFPEPVTVSWNSGALTSG---VHTPPAVL-----QSSGLYSLSSV 211
 Qy 91 VNITQGMSSNTYTCVHKH---NGSIFEDSSRRCSDDP-----RGVITYLIPPSPL 140
 Db 212 VVTSSNP-GTQTYTCNVDRKPSNTKVDKTVKCKVCCPCPAPVAGPSVFLFPKPK 270
 Qy 141 D-LYENGTPKLTCLVLDLESEE-NITVTWVRERKKSIGASQSTKHHHATTSITSLPV 198
 Db 271 DTLMSRTPETVTCVVVDVSHEDPEVFQFNWYDGMVHNAKTPREEQFNSTFRVVSULTV 330
 Qy 199 DAKDWIEGEGQCRVDHPFPKPIVRSITKLPGKRLAPEVYMLPPSPPE-TGTTTRVTCL 257
 Db 331 VHQDWLNGKEYCKKSNKGLPAPIETKISKTKGQPREQVYTLPPSREEMTKNQVSLTCL 390
 Qy 258 IRGFYPSISVQWLPNNEDHTGHTHTTRPQKDHGTDPSFFLYSRMLVKNKSIWEKGNLVT 317
 Db 391 VKGFYPSIDIAWESNGQPEN--NYKTTTPMLD--SDGSFFLYSKLTVDKSRWQQGNVFS 446

Qy 318 CRVVEALPGSRITLEKSLHYSAG 340
 Db 447 CSVMHEALHNHYT-QKSLSLSPG 468

Db 447 CSVMEALHNHYT-QKSLSLSPG 468

RESULT 14

US-08-477-460B-4

; Sequence 4, Application US/08477460B

; Patent No. 6034223

; GENERAL INFORMATION:

; APPLICANT: Progenics Pharmaceuticals, Inc.

; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED

; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/477,460B

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/927,931

; FILING DATE: 07-AUG-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 977-9550

; TELEFAX: (212) 977-9809

; TELEX: 422523 COOP UI

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 530 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: homo sapien

; CELL TYPE: lymphocyte

US-08-477-460B-4

Query Match 25.3%; Score 469.5; DB 3; Length 530;

Best Local Similarity 32.8%; Pred. No. 2.6e-38;

Matches 121; Conservative 68; Mismatches 129; Indels 51; Gaps 14;

Qy 10 LSLPESGPVTI-----IPPTVKLFHSSCDP-----RGDAHTIQLLCIV 48

Db 174 LELQDSGTWCTVLQNKQKVEFKIDIVLAFASFKGVSFPLAPCSRSTSESTAALGCLV 233

Qy 49 SGFSPAKVHVTVW-----LVDQGEAENLFPYTRPKREGGQTFSLQSEVNITQGWMSNTY 104

Db 234 KDYPPEPVTVSNWNSGALTSG---VHTFFPAVL-----QSSGLYSLSSVVTVPPSSNF-GTQTY 285

Qy 105 TCHVKH---NGSIFEDSSRRCSDDP-----RGVITYLIPPSPLD-LYENGTPKLTCL 153

Db 286 TCNVDPKPSNTKVDKTVKRCCEPCPCPAPVAGSVFLFPKPKDTLMISRTPEVTCV 345

Qy 154 VLDLSEEE-NITVTWVRERKKSIGSASQSRSTKHHATTSTISILPVDADKWIEGEGYQCR 212

Db 346 VVDVSHEDPEVQFNWYVDGVEVHNAKTKPREBEQFNSTFRVWSVLTVVHQDWLNGKEYCK 405

Qy 213 VDPHPFKPIVRSITKLPCKRLAPEVYMLPPSPPEE-TGTRTVTCLIRGFYSEISVOWL 271

Db 406 VSNKGLPAPIEKTISTKTGQPREPQVYTLPPSREMTKNQVSLTCLVKGYFSPDIAVEWE 465

Qy 272 PNNEEDHTGHTTTRPQKHGTDPSFFLYSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTL 331

Db 466 SNGQPEN--NYKTTTPPMLD--SDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYT- 520

Qy 332 EKSLHYSAG 340

Db 521 QKSLSLSPG 529

Db 521 QKSLSLSPG 529

Db 521 QKSLSLSPG 529

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Search completed: March 8, 2003, 07:50:33

Job time : 21 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 8, 2003, 07:49:30 ; Search time 17 Seconds
(without alignments)
845.884 Million cell updates/sec

Title: US-09-401-636-4
Perfect score: 1858
Sequence: 1 EPHHHHHHTLSLPESGPVTI.....HEALPGSRTLEKSLHYSAGN 341

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues
Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1858	100.0	341	9	US-10-176-664-4
2	1858	100.0	341	10	US-09-401-636-4
3	1840	99.0	341	9	US-10-176-664-9
4	1840	99.0	341	10	US-09-401-636-9
5	1720	92.6	341	9	US-10-176-664-6
6	1720	92.6	341	10	US-09-401-636-6
7	1691.5	91.0	342	9	US-10-176-664-5
8	1691.5	91.0	342	10	US-09-401-636-5
9	1595	85.8	341	9	US-10-176-664-11
10	1595	85.8	341	10	US-09-401-636-11
11	1555	83.7	345	9	US-10-176-664-10
12	1555	83.7	345	10	US-09-401-636-10
13	1553.5	83.6	342	9	US-10-176-664-8
14	1553.5	83.6	342	10	US-09-401-636-8
15	1529	82.3	341	9	US-10-176-664-3
16	1529	82.3	341	10	US-09-401-636-3
17	1051	56.6	340	9	US-10-176-664-2
18	1051	56.6	340	10	US-09-401-636-2
19	1025	55.2	343	9	US-10-176-664-7

20	1025	55.2	343	10	US-09-401-636-7	Sequence 7, Appli
21	940.5	50.6	421	9	US-09-949-375A-28	Sequence 28, Appl
22	936	50.4	332	9	US-09-949-375A-23	Sequence 23, Appl
23	936	50.4	332	9	US-09-949-375A-25	Sequence 25, Appl
24	936	50.4	332	9	US-09-949-375A-27	Sequence 27, Appl
25	931.5	50.1	431	9	US-09-479-614-14	Sequence 14, Appl
26	931.5	50.1	496	9	US-09-479-614-2	Sequence 2, Appli
27	931.5	50.1	496	9	US-09-479-614-29	Sequence 29, Appl
28	929.5	50.0	432	9	US-09-949-375A-19	Sequence 19, Appl
29	925	49.8	343	9	US-09-949-375A-20	Sequence 20, Appl
30	925	49.8	343	9	US-09-949-375A-22	Sequence 22, Appl
31	745	40.1	323	9	US-09-949-375A-2	Sequence 2, Appli
32	745	40.1	323	9	US-09-949-375A-4	Sequence 4, Appli
33	745	40.1	323	9	US-09-949-375A-6	Sequence 6, Appli
34	745	40.1	331	9	US-10-176-664-1	Sequence 1, Appli
35	745	40.1	331	10	US-09-401-636-1	Sequence 1, Appli
36	745	40.1	428	9	US-10-047-542-60	Sequence 60, Appl
37	745	40.1	428	9	US-09-949-375A-1	Sequence 1, Appli
38	745	40.1	428	10	US-09-316-230-1	Sequence 1, Appli
39	745	40.1	574	9	US-10-047-542-45	Sequence 45, Appl
40	743	40.0	330	9	US-09-949-375A-10	Sequence 10, Appl
41	741	39.9	336	9	US-09-949-375A-8	Sequence 8, Appli
42	741	39.9	441	9	US-09-949-375A-7	Sequence 7, Appli
43	526	28.3	352	9	US-09-828-995B-38	Sequence 38, Appl
44	525	28.3	470	9	US-09-828-995B-11	Sequence 11, Appl
45	520.5	28.0	468	9	US-09-828-995B-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-176-664-4
; Sequence 4, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-4

Query Match	100.0%	Score	1858;	DB	9;	Length	341;
Best Local Similarity	100.0%	Pred. No.	2e-122;				
Matches	341;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	EPHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW	60				
Db	1	EPHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW	60				
Qy	61	LVDGQAEHLPPYTRPKREGQTSLOSEVNITGQWMSNTYTCHVKHNGSIFEDSSR	120				
Db	61	LVDGQAEHLPPYTRPKREGQTSLOSEVNITGQWMSNTYTCHVKHNGSIFEDSSR	120				
Qy	121	RCSDDPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVTWVRKKSGSASQ	180				
Db	121	RCSDDPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVTWVRKKSGSASQ	180				
Qy	181	RSTKHHHTTSITSLPVDADKWISGEGYQCQVDHHPHPKPIVRSITKLPGRKLAPEVYM	240				
Db	181	RSTKHHHTTSITSLPVDADKWISGEGYQCQVDHHPHPKPIVRSITKLPGRKLAPEVYM	240				

Db 181 RSTKHHHTTSLPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 240
Qy 241 LPPSPETGTTTTCVCLIRGFPSEISVQWLPNNEEDHTGHTTTRPQKHGTDPSFFLY 300
Db 241 LPPSPETGTTTTCVCLIRGFPSEISVQWLPNNEEDHTGHTTTRPQKHGTDPSFFLY 300
Qy 301 SRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 SRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 2

US-09-401-636-4
; Sequence 4, Application US/09401636
; Patent No. US2001003843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-4

Query Match 100.0%; Score 1858; DB 10; Length 341;
Best Local Similarity 100.0%; Pred. No. 2e-122;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EFHHHHHTLSPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Qy 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNIQTQWMSNTYTCHVKHNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNIQTQWMSNTYTCHVKHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLESEENITVTVWRERKKSIGSASQ 180
Db 121 RCDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLESEENITVTVWRERKKSIGSASQ 180
Qy 181 RSTKHHHTTSLPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 240
Db 181 RSTKHHHTTSLPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 240
Qy 241 LPPSPETGTTTTCVCLIRGFPSEISVQWLPNNEEDHTGHTTTRPQKHGTDPSFFLY 300
Db 241 LPPSPETGTTTTCVCLIRGFPSEISVQWLPNNEEDHTGHTTTRPQKHGTDPSFFLY 300
Qy 301 SRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 SRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 3

US-10-176-664-9
; Sequence 9, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636

; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-9

Query Match 99.0%; Score 1840; DB 9; Length 341;
Best Local Similarity 99.4%; Pred. No. 3.6e-121;
Matches 339; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EFHHHHHTLSPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Qy 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNIQTQWMSNTYTCHVKHNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNIQTQWMSNTYTCHVKHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLESEENITVTVWRERKKSIGSASQ 180
Db 121 RCDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLESEENITVTVWRERKKSIGSASQ 180
Qy 181 RSTKHHHTTSLPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 240
Db 181 RSTKHHHTTSLPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 240
Qy 241 LPPSPETGTTTTCVCLIRGFPSEISVQWLPNNEEDHTGHTTTRPQKHGTDPSFFLY 300
Db 241 LPPSPETGTTTTCVCLIRGFPSEISVQWLPNNEEDHTGHTTTRPQKHGTDPSFFLY 300
Qy 301 SRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 SRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 4

US-09-401-636-9
; Sequence 9, Application US/09401636
; Patent No. US2001003843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-9

Query Match 99.0%; Score 1840; DB 10; Length 341;
Best Local Similarity 99.4%; Pred. No. 3.6e-121;
Matches 339; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EFHHHHHTLSPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Qy 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNIQTQWMSNTYTCHVKHNGSIFEDSSR 120

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1
Db 61 LVDGQAEANLFPYTRPKREGGQTSFLOSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180
Db 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180
Qy 181 RSTKHHATTSTISILPVDADKWIIEGEGYQCRVDHPHFKPIVRSITKLPGRKLAPEVY 240
Db 181 RSTKHHATTSTISILPVDADKWIIEGEGYQCRVDHPHFKPIVRSITKLPGRKLAPEVY 240
Qy 241 LPPSPDEETGTRTTCCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKQKHGTDPSPFL 300
Db 241 LPPSPDEETGTRTTCCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKQKHGTDPSPFL 300
Qy 301 SRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 SRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 5
US-10-176-664-6
; Sequence 6, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins

Query Match 92.6%; Score 1720; DB 9; Length 341;
Best Local Similarity 93.3%; Pred. No. 8.3e-113;
Matches 319; Conservative 9; Mismatches 12; Indels 2; Gaps 2;

Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Qy 61 LVDGQAEANLFPYTRPKREGGQTSFLOSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPKREGGQTSFLOSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180
Db 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180
Qy 181 RSTKHH-HATTSTISILPVDADKWIIEGEGYQCRVDHPHFKPIVRSITKLPGRKLAPEVY 239
Db 181 RSTKHH-HATTSTISILPVDADKWIIEGEGYQCRVDHPHFKPIVRSITKLPGRKLAPEVY 239
Qy 240 MLPPSPDEETGTRTTCCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKQKHGTDPSPFL 299
Db 240 MLPPSPDEETGTRTTCCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKQKHGTDPSPFL 299
Qy 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 7
US-10-176-664-5
; Sequence 5, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
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RESULT 6
US-09-401-636-6
; Sequence 6, Application US/09401636
; Patent No. US2001003843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins

US-09-401-636-6
Query Match 92.6%; Score 1720; DB 10; Length 341;
Best Local Similarity 93.3%; Pred. No. 8.3e-113;
Matches 319; Conservative 9; Mismatches 12; Indels 2; Gaps 2;

Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Qy 61 LVDGQAEANLFPYTRPKREGGQTSFLOSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPKREGGQTSFLOSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180
Db 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180
Qy 181 RSTKHH-HATTSTISILPVDADKWIIEGEGYQCRVDHPHFKPIVRSITKLPGRKLAPEVY 239
Db 181 RSTKHH-HATTSTISILPVDADKWIIEGEGYQCRVDHPHFKPIVRSITKLPGRKLAPEVY 239
Qy 240 MLPPSPDEETGTRTTCCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKQKHGTDPSPFL 299
Db 240 MLPPSPDEETGTRTTCCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKQKHGTDPSPFL 299
Qy 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 7
US-10-176-664-5
; Sequence 5, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
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US-10-176-664-5

Query Match 91.0%; Score 1691.5; DB 9; Length 342;
Best Local Similarity 90.9%; Pred. No. 8.1e-111;
Matches 311; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
Qy 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRKKSIGSASQ 180
Db 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRKKSIGSARS 180
Qy 181 RSTK-HHHATTSTISLPVDAKDWIEGEGYQCRVDHPHPKPIVRSITKLPKRLAPEVY 239
Db 181 LVVKEQYNGTFTVSHLPVNTDWDIEGTYTCRLSPDMPYPLIRIISKAPKRLAPEVY 240
Qy 240 MLPSPPEETGTRTTCVCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKDGHGTDPSFFL 299
Db 241 MLPSPPEETGTRTTCVCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKDGHGTDPSFFL 300
Qy 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342

RESULT 8

US-09-401-636-5
; Sequence 5, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-5

Query Match 91.0%; Score 1691.5; DB 10; Length 342;
Best Local Similarity 90.9%; Pred. No. 8.1e-111;
Matches 311; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
Qy 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRKKSIGSASQ 180
Db 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRKKSIGSARS 180
Qy 181 RSTK-HHHATTSTISLPVDAKDWIEGEGYQCRVDHPHPKPIVRSITKLPKRLAPEVY 239
Db 181 LVVKEQYNGTFTVSHLPVNTDWDIEGTYTCRLSPDMPYPLIRIISKAPKRLAPEVY 240

Qy 240 MLPSPPEETGTRTTCVCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKDGHGTDPSFFL 299
Db 241 MLPSPPEETGTRTTCVCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKDGHGTDPSFFL 300
Qy 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342

RESULT 9

US-10-176-664-11
; Sequence 11, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-11

Query Match 85.8%; Score 1595; DB 9; Length 341;
Best Local Similarity 85.0%; Pred. No. 4.3e-104;
Matches 290; Conservative 16; Mismatches 35; Indels 0; Gaps 0;

Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
Qy 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRKKSIGSASQ 180
Db 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRKKSIGSASQ 180
Qy 181 RSTKHHATTSTISLPVDAKDWIEGEGYQCRVDHPHPKPIVRSITKLPKRLAPEVW 240
Db 181 NKDHFNGTITVTSTLPVNTDWDIEGTYTCRVTHPHLPKDIVRSIAKLPKRLAPEVW 240
Qy 241 LPPSPPEETGTRTTCVCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKDGHGTDPSFFLY 300
Db 241 LPPSPPEETGTRTTCVCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKDGHGTDPSFFLY 300
Qy 301 SRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 SRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 10

US-09-401-636-11
; Sequence 11, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652


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; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-11

Query Match      85.8%; Score 1595; DB 10; Length 341;
Best Local Similarity 85.0%; Pred. No. 4.3e-104;
Matches 290; Conservative 16; Mismatches 35; Indels 0; Gaps 0;

Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60

Qy 61 LVDQEAENLFPYTRPKREGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120
Db 61 LVDQEAENLFPYTRPKREGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120

Qy 121 RCSDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLESEENITVTVRERKKSIGSASQ 180
Db 121 RCSDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLESEENITVTVRERKKSIGSASQ 180

Qy 121 KCSSEDPKGVTSYLSPPSPDLVYHKAPTICLVVDLATMGMNLTWYRESKEPVNPGPL 180
Db 121 KCSSEDPKGVTSYLSPPSPDLVYHKAPTICLVVDLATMGMNLTWYRESKEPVNPGPL 180

Qy 181 RSTKHHTTITSILPVDADKDWIEGEGYQCRVDHPFPKPIVRSITKLPKRLAPEVYM 240
Db 181 NKQDFNGTIVTSLPVTNDWIEGEYTCRVTHPLPKDIVRSIAKLPKRLAPEVYM 240

Qy 241 LPPSPETGTRTTCVLRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPSPFLY 300
Db 241 LPPSPETGTRTTCVLRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPSPFLY 300

Qy 301 SRMLVNKSIWEKGNLVTCTVVRVVEALPGSRTLEKSLHYSAGN 341
Db 301 SRMLVNKSIWEKGNLVTCTVVRVVEALPGSRTLEKSLHYSAGN 341

RESULT 11
US-10-176-664-10
; Sequence 10, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-10-176-664-10

Query Match      83.7%; Score 1555; DB 9; Length 345;
Best Local Similarity 84.1%; Pred. No. 2.7e-101;
Matches 290; Conservative 13; Mismatches 38; Indels 4; Gaps 2;

Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60

Qy 61 LVDQEAENLFPYTRPKREGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120
Db 61 LVDQEAENLFPYTRPKREGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120

Qy 121 RCSDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLESEENITVTVRERKKSIGSASQ 180
Db 121 RCSDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLESEENITVTVRERKKSIGSASQ 180

Qy 181 RSTKHHTTITSILPVDADKDWIEGEGYQCRVDHPFPKPIVRSITKLPKRLAPEVYM 240
Db 181 NKQDFNGTIVTSLPVTNDWIEGEYTCRVTHPLPKDIVRSIAKLPKRLAPEVYM 240

Qy 241 LPPSPETGTRTTCVLRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPSPFLY 300
Db 241 LPPSPETGTRTTCVLRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPSPFLY 300

Qy 301 SRMLVNKSIWEKGNLVTCTVVRVVEALPGSRTLEKSLHYSAGN 341
Db 301 SRMLVNKSIWEKGNLVTCTVVRVVEALPGSRTLEKSLHYSAGN 341

RESULT 12
US-09-401-636-10
; Sequence 10, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-10

Query Match      83.7%; Score 1555; DB 10; Length 345;
Best Local Similarity 84.1%; Pred. No. 2.7e-101;
Matches 290; Conservative 13; Mismatches 38; Indels 4; Gaps 2;

Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60

Qy 61 LVDQEAENLFPYTRPKREGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120
Db 61 LVDQEAENLFPYTRPKREGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120

Qy 121 RCSDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLESEENITVTVRERKKSIGSASQ 180
Db 121 RCSDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLESEENITVTVRERKKSIGSASQ 180

Qy 181 RSTKHHTTITSILPVDADKDWIEGEGYQCRVDHPFPKPIVRSITKLPKRLAPEVYM 240
Db 181 NKQDFNGTIVTSLPVTNDWIEGEYTCRVTHPLPKDIVRSIAKLPKRLAPEVYM 240

Qy 241 LPPSPETGTRTTCVLRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPSPFLY 300
Db 241 LPPSPETGTRTTCVLRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPSPFLY 300

Qy 301 SRMLVNKSIWEKGNLVTCTVVRVVEALPGSRTLEKSLHYSAGN 341
Db 301 SRMLVNKSIWEKGNLVTCTVVRVVEALPGSRTLEKSLHYSAGN 341

RESULT 13
US-10-176-664-8
; Sequence 10, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-10-176-664-10

Query Match      83.7%; Score 1555; DB 9; Length 345;
Best Local Similarity 84.1%; Pred. No. 2.7e-101;
Matches 290; Conservative 13; Mismatches 38; Indels 4; Gaps 2;

Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60

Qy 61 LVDQEAENLFPYTRPKREGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120
Db 61 LVDQEAENLFPYTRPKREGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120
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Db 61 LVDQEAENLFPYTRPKREGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120
Qy 121 RC-SDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLESEENITVTVRERKKSIGSASQ 176
Db 121 RCTAESPGRGVSAVLSPPPTPLDLYVHKSPKLTCLVLDLASSENVNLLWSRKNKGVIILPP 180
Qy 177 SASORSTKHHHTTITSILPVDADKDWIEGEGYQCRVDHPFPKPIVRSITKLPKRLAPE 236
Db 181 PGPPVIKPOFNGTFSATSTLFPVNSVDWIEGEYTCRVTHPLPKDIVRSIAKLPKRLAPE 240
Qy 237 EYVMLPPSPETGTRTTCVLRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPSPFLY 296
Db 241 EYVMLPPSPETGTRTTCVLRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPSPFLY 300
Qy 297 FFLYSRMLVNKSIWEKGNLVTCTVVRVVEALPGSRTLEKSLHYSAGN 341
Db 301 FFLYSRMLVNKSIWEKGNLVTCTVVRVVEALPGSRTLEKSLHYSAGN 341

RESULT 12
US-09-401-636-10
; Sequence 10, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-10

Query Match      83.7%; Score 1555; DB 10; Length 345;
Best Local Similarity 84.1%; Pred. No. 2.7e-101;
Matches 290; Conservative 13; Mismatches 38; Indels 4; Gaps 2;

Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60

Qy 61 LVDQEAENLFPYTRPKREGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120
Db 61 LVDQEAENLFPYTRPKREGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120

Qy 121 RC-SDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLESEENITVTVRERKKSIGSASQ 176
Db 121 RCTAESPGRGVSAVLSPPPTPLDLYVHKSPKLTCLVLDLASSENVNLLWSRKNKGVIILPP 180
Qy 177 SASORSTKHHHTTITSILPVDADKDWIEGEGYQCRVDHPFPKPIVRSITKLPKRLAPE 236
Db 181 PGPPVIKPOFNGTFSATSTLFPVNSVDWIEGEYTCRVTHPLPKDIVRSIAKLPKRLAPE 240
Qy 237 EYVMLPPSPETGTRTTCVLRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPSPFLY 296
Db 241 EYVMLPPSPETGTRTTCVLRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPSPFLY 300
Qy 297 FFLYSRMLVNKSIWEKGNLVTCTVVRVVEALPGSRTLEKSLHYSAGN 341
Db 301 FFLYSRMLVNKSIWEKGNLVTCTVVRVVEALPGSRTLEKSLHYSAGN 341

RESULT 13
US-10-176-664-8
; Sequence 10, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-10-176-664-8
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; Sequence 8, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-10-176-664-8

Query Match      83.6%; Score 1553.5; DB 9; Length 342;
Best Local Similarity 82.7%; Pred. No. 3.3e-101;
Matches 283; Conservative 21; Mismatches 37; Indels 1; Gaps 1;

Qy 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60
Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60

Qy 61 LVDQEAENLFPYTRPKREGQTFSLQSEVNIITOGQWSSNTYTCHVKHNGSIFEDSSR 120
Db 61 LVDQEAENLFPYTRPKREGQTFSLQSEVNIITOGQWSSNTYTCHVKHNGSIFEDSSR 120

Qy 121 RCDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDL-ESEENITVTWVRERKKSIGSAS 179
Db 121 RCDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDL-ESEENITVTWVRERKKSIGSAS 179

Qy 180 QRSTKHHTATTSITSLPVDADKWIEGEGYQCRVDHPPKPIVRSITKLPKRLAPEVY 239
Db 180 QRSTKHHTATTSITSLPVDADKWIEGEGYQCRVDHPPKPIVRSITKLPKRLAPEVY 239

Qy 240 MLPSPPEETGTRTTCCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKDGHGTDPSFPL 299
Db 240 MLPSPPEETGTRTTCCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKDGHGTDPSFPL 299

Qy 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342

RESULT 15
US-10-176-664-3
; Sequence 3, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-10-176-664-3

Query Match      82.3%; Score 1529; DB 9; Length 341;
Best Local Similarity 80.6%; Pred. No. 1.7e-99;
Matches 275; Conservative 28; Mismatches 38; Indels 0; Gaps 0;

Qy 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60
Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60

Qy 61 LVDQEAENLFPYTRPKREGQTFSLQSEVNIITOGQWSSNTYTCHVKHNGSIFEDSSR 120
Db 61 LVDQEAENLFPYTRPKREGQTFSLQSEVNIITOGQWSSNTYTCHVKHNGSIFEDSSR 120

Qy 121 RCDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDL-ESEENITVTWVRERKKSIGSASQ 180
Db 121 RCDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDL-ESEENITVTWVRERKKSIGSASQ 180

Qy 181 RSTKHHTATTSITSLPVDADKWIEGEGYQCRVDHPPKPIVRSITKLPKRLAPEVY 240
Db 181 RSTKHHTATTSITSLPVDADKWIEGEGYQCRVDHPPKPIVRSITKLPKRLAPEVY 240

Qy 181 VVKEQYNGTFTVTSHLPVNTDDWIEGDTYTCRLSPDMFVPLIRTISKAPGKRLAPEVYM 240
Db 181 VVKEQYNGTFTVTSHLPVNTDDWIEGDTYTCRLSPDMFVPLIRTISKAPGKRLAPEVYM 240
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Qy 241 LPPSPETGTTTTCCLIRGYPSEISVQWLPNNNEEDTGHHTTTRPQKHGTDPSFELY 300
Db 241 LPPSPETGTTTTCCLIRGYPSEISVQWLPNNNEEDTGHHTTTRPQKHGTDPSFELY 300
Qy 301 SRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 SRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341

Search completed: March 8, 2003, 07:54:18
Job time : 18 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 8, 2003, 07:43:00 ; Search time 38 Seconds
(without alignments)
1195.749 Million cell updates/sec

Title: US-09-401-636-4

Perfect score: 1958

Sequence: 1 EPHHHHTLSLPESGPVTI.....HEALPGSRTLEKSLHVSAGN 341

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1840	99.0	341	21	Immunogenic peptid
2	1595	85.8	341	21	Immunogenic peptid
3	1555	83.7	345	21	Immunogenic peptid
4	1533.5	83.6	342	21	Immunogenic peptid
5	1539	82.8	341	21	Immunogenic peptid
6	1526	82.1	341	21	Opossum IGE heavy
7	1511.5	81.4	342	21	Immunogenic peptid
8	1051	56.6	340	21	Rat IGE heavy chain
9	1012	54.5	313	21	Rat immunoglobulin
10	973	52.4	343	21	Platyus IGE heavy

11	940.5	50.6	421	23	AAU80300	Mouse IGE heavy ch
12	938.5	50.5	426	17	AAU97753	Canine IGE. Canis
13	936	50.4	332	23	AAU80297	Mouse IGE heavy ch
14	936	50.4	332	23	AAU80298	Murine IGE heavy c
15	935	50.4	332	23	AAU80299	Murine IGE heavy c
16	934.5	50.3	417	18	AAW23067	Canine IGE heavy c
17	929.5	50.0	432	23	AAU80294	Murine IGE heavy c
18	925	49.8	343	23	AAU80295	Murine IGE heavy c
19	925	49.8	343	23	AAU80296	Murine IGE heavy c
20	922.5	49.7	312	21	AAV79995	Dog immunoglobulin
21	898	48.3	424	23	AAW50103	Equine IGE heavy c
22	896	48.2	424	23	AAW50104	Equine IGE heavy c
23	862.5	46.4	561	20	AAV17415	Mouse immunoglobul
24	847	45.6	313	21	AAV79997	Mouse immunoglobul
25	745	40.1	323	23	AAU80284	Human IGE heavy ch
26	745	40.1	323	23	AAU80285	Human IGE C2-C3-C4
27	745	40.1	323	23	AAU80286	Human IGE C2-C3-C4
28	745	40.1	324	16	AAW33559	Fc(epsilon) CH2'-C
29	745	40.1	325	16	AAW75225	Human IGE Fc chain
30	745	40.1	325	16	AAW77241	Human IGE Fc chain
31	745	40.1	331	21	AAW33642	Human IGE heavy ch
32	745	40.1	367	9	AAW80291	Interleukin-2/IGE
33	745	40.1	428	23	AAU80283	Human IGE heavy ch
34	745	40.1	428	23	AAW50940	Human IGE epsilon
35	745	40.1	428	23	AAW47863	Human IGE heavy c
36	743	40.0	330	23	AAU80289	Human IGE C2-C3-C4
37	742	39.9	325	21	AAV79994	Human immunoglobul
38	741	39.9	325	16	AAW83582	CH2 to CH4 of huma
39	741	39.9	336	23	AAU80288	Human IGE heavy ch
40	741	39.9	441	23	AAU80287	Human IGE heavy ch
41	737	39.7	493	5	AAW40065	Sequence of human
42	726	39.1	315	16	AAW85582	Fc(epsilon) CH2' -C
43	709	38.2	428	14	AAW42950	Human IGE heavy ch
44	525.5	28.3	245	14	AAW38858	Anti-allergic chim
45	520.5	28.0	468	22	AAU69120	Canine IGE heavy c

ALIGNMENTS

RESULT 1

AAW6206
ID AAW6206 standard; protein; 341 AA.

AC AAW6206;

DT 22-NOV-2000 (first entry)

DE Immunogenic peptide consisting of opossum CH2, rat CH3 and opossum CH4.

KW Rat; opossum; immunoglobulin E; IGE; vaccination; infection; allergy;

KW asthma; eczema; immunogenic peptide.

OS Chimeric - Didelphis virginiana.

OS Chimeric - Rattus sp.

PN WO200025722-A2.

PD 11-MAY-2000.

XX 21-OCT-1999; 99WO-SE01896.

XX 02-NOV-1998; 98US-0106652.

XX 22-SEP-1999; 99US-0401636.

XX (RESI-) RESISTENTIA PHARM AB.

XX Hellman LT;

XX WPI; 2000-365342/31.

XX Immunogenic polypeptides useful for preventing the harmful effects of

PT immunoglobulin E in mammals -

XX Disclosure; Fig 2; 50pp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy

CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain

CC constant region 3 from the rat. It was shown to cause a stronger

CC polyclonal anti-self IgE response than peptides consisting of the same

CC regions from one mammal. Immunogenic peptides, particularly those

CC consisting of different heavy chain constant regions, can be used for

CC vaccination in humans, against bacterial and viral infections and

CC allergies, such as asthma, fur, pollen and food allergies and eczema.

XX Sequence 341 AA;

XX Query Match 99.0%; Score 1840; DB 21; Length 341;

XX Best Local Similarity 99.4%; Pred. No. 1.8e-144;

XX Matches 339; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPHHHHHHTLSLPSGPGVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60

Db 1 EPHHHHHHTLSLPSGPGVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60

Qy 61 LVDGQEAENLFYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120

Db 61 LVDGQEAENLFYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120

Qy 121 RCDDEPRGVITLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180

Db 121 RCDDEPRGVITLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180

Qy 181 RSTKHHAHTTSITSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVW 240

Db 181 RSTKHHAHTTSITSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVW 240

Qy 241 LPPSPETGTRTCTVCLIRGFYFSEISVQWLPNNEEDHTGHTTTRPKDHTGDPSPFLY 300

Db 241 LPPSPETGTRTCTVCLIRGFYFSEISVQWLPNNEEDHTGHTTTRPKDHTGDPSPFLY 300

Qy 301 SRMLVNKSIWEKGNLVCRTVCRVVEALPGSRTLEKSLHYSAGN 341

Db 301 SRMLVNKSIWEKGNLVCRTVCRVVEALPGSRTLEKSLHYSAGN 341

RESULT 2

AAB06208

ID AAB06208 standard; protein; 341 AA.

XX AAB06208;

XX AC AAB06208;

XX DT 22-NOV-2000 (first entry)

XX Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.

XX Dog; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;

XX asthma; eczema; immunogenic peptide.

XX Chimeric - Didelphis virginiana.

XX Chimeric - Canis sp.

XX WO200025722-A2.

XX 11-MAY-2000.

XX 21-OCT-1999; 99WO-SE01896.

XX 02-NOV-1998; 98US-0106652.

XX 22-SEP-1999; 99US-0401636.

XX (RESI-) RESISTENTIA PHARM AB.

XX Hellman LT;

XX WPI; 2000-365342/31.

XX Immunogenic polypeptides useful for preventing the harmful effects of

PT immunoglobulin E in mammals -

XX Disclosure; Fig 2; 50pp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy

CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain

CC constant region 3 from the dog. It was shown to cause a stronger

CC polyclonal anti-self IgE response than peptides consisting of the same

CC regions from one mammal. Immunogenic peptides, particularly those

CC consisting of different heavy chain constant regions, can be used for

CC vaccination in humans, against bacterial and viral infections and

CC allergies, such as asthma, fur, pollen and food allergies and eczema.

XX Sequence 341 AA;

XX Query Match 85.8%; Score 1595; DB 21; Length 341;

XX Best Local Similarity 85.0%; Pred. No. 3.8e-124;

XX Matches 290; Conservative 16; Mismatches 35; Indels 0; Gaps 0;

Qy 1 EPHHHHHHTLSLPSGPGVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60

Db 1 EPHHHHHHTLSLPSGPGVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60

Qy 61 LVDGQEAENLFYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120

Db 61 LVDGQEAENLFYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120

Qy 121 RCDDEPRGVITLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180

Db 121 RCDDEPRGVITLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180

Qy 181 RSTKHHAHTTSITSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVW 240

Db 181 NKDHFNGTITVSTLPTVNTDNDIEGETTYCRVTHPLPKDIVRSIAKLPGRKLAPEVW 240

Qy 241 LPPSPETGTRTCTVCLIRGFYFSEISVQWLPNNEEDHTGHTTTRPKDHTGDPSPFLY 300

Db 241 LPPSPETGTRTCTVCLIRGFYFSEISVQWLPNNEEDHTGHTTTRPKDHTGDPSPFLY 300

Qy 301 SRMLVNKSIWEKGNLVCRTVCRVVEALPGSRTLEKSLHYSAGN 341

Db 301 SRMLVNKSIWEKGNLVCRTVCRVVEALPGSRTLEKSLHYSAGN 341

RESULT 3

AAB06207

ID AAB06207 standard; protein; 345 AA.

XX AAB06207;

XX AC AAB06207;

XX DT 22-NOV-2000 (first entry)

XX Immunogenic peptide consisting of opossum CH2, pig CH3 and opossum CH4.

XX Pig; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;

XX asthma; eczema; immunogenic peptide.

XX Chimeric - Didelphis virginiana.

XX Chimeric - Sus scrofa.

XX WO200025722-A2.

XX 11-MAY-2000.

XX 21-OCT-1999; 99WO-SE01896.

XX 02-NOV-1998; 98US-0106652.

XX 22-SEP-1999; 99US-0401636.

XX (RESI-) RESISTENTIA PHARM AB.

XX Hellman LT;

XX WPI; 2000-365342/31.

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PI Hellman LT;
XX WPI; 2000-365342/31.
XX Immunogenic polypeptides useful for preventing the harmful effects of
XX immunoglobulin E in mammals -
XX Disclosure; Fig 2; 50pp; English.
XX The present sequence is an immunogenic peptide consisting of the heavy
XX chain constant regions 2 and 4 of the opossum IGE and the heavy chain
XX constant region 3 from the pig. It was shown to cause a stronger
XX polyclonal anti-self IGE response than peptides consisting of the same
XX regions from one mammal. Immunogenic peptides, particularly those
XX consisting of different heavy chain constant regions, can be used for
XX vaccination in humans, against bacterial and viral infections and
XX allergies, such as asthma, fur, pollen and food allergies and eczema.
XX Sequence 345 AA;
Query Match 83.7%; Score 1555; DB 21; Length 345;
Best Local Similarity 84.1%; Pred. No. 8e-121;
Matches 290; Conservative 13; Mismatches 38; Indels 4; Gaps 2;
Qy 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
Qy 61 LVDGQEAENLPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSR 120
Db 61 LVDGQEAENLPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSR 120
Qy 121 RC-SDEPRGVITYLIPSPDLXENGTPKLTCLVLDLSEENITVTWVRKKSI---G 176
Db 121 RCTAESEPRGVSAYLSPPTPLDLYHKSPKLTCLVLDLSEENITVTWVRKKSI---G 176
Qy 177 SASQRSTKHHTATSIILPVDADKWIEGEGYQCRVDHPFPKPIVRSITKLPGRLAPEV 236
Db 181 PGPPVVKPQFGTFSATSLPVDVSDWIEGETTYCNVTHPDLPKPILRSISKLPGRILAP 240
Qy 237 EYMLPPSPETGTRTTCCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDP 296
Db 241 EYMLPPSPETGTRTTCCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDP 300
Qy 297 FFLYSRMLVNKSIWEKGNLTCRVVHEALPGSRTLKSLHYSAGN 341
Db 301 FFLYSRMLVNKSIWEKGNLTCRVVHEALPGSRTLKSLHYSAGN 345
RESULT 4
AAB06205
ID AAB06205 standard; protein; 342 AA.
XX AC AAB06205;
XX AC AAB06205;
XX DT 22-NOV-2000 (first entry)
XX DE Immunogenic peptide consisting of opossum CH2, human CH3 and opossum CH4.
XX KW Human; opossum; immunoglobulin E; IGE; vaccination; infection; allergy;
XX KW asthma; eczema; immunogenic peptide.
XX OS Chimeric - Didelphis virginiana.
XX OS Chimeric - Homo sapiens.
XX PN WO200025722-A2.
XX XX
XX FD 11-MAY-2000.
XX XX
XX PF 21-OCT-1999; 99WO-SE01896.
XX XX
XX PR 02-NOV-1998; 98US-0106652.
XX PR 22-SEP-1999; 99US-0401636.
XX PR
XX PA (RESI-) RESISTENTIA PHARM AB.
XX PI Hellman LT;
XX DR WPI; 2000-365342/31.
XX PT Immunogenic polypeptides useful for preventing the harmful effects of
XX PT immunoglobulin E in mammals -
XX PS Disclosure; Fig 2; 50pp; English.
XX XX
XX XX The present sequence is an immunogenic peptide consisting of the heavy
XX chain constant regions 2 and 4 of the opossum IGE and the heavy chain
XX constant region 3 from the human. It was shown to cause a stronger
XX polyclonal anti-self IGE response than peptides consisting of the same
XX regions from one mammal. Immunogenic peptides, particularly those
XX consisting of different heavy chain constant regions, can be used for
XX vaccination in humans, against bacterial and viral infections and
XX allergies, such as asthma, fur, pollen and food allergies and eczema.
XX Sequence 342 AA;
Query Match 83.6%; Score 1553.5; DB 21; Length 342;
Best Local Similarity 82.7%; Pred. No. 1.1e-120;
Matches 283; Conservative 21; Mismatches 37; Indels 1; Gaps 1;
Qy 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
Qy 61 LVDGQEAENLPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSR 120
Db 61 LVDGQEAENLPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSR 120
Qy 121 RCSDDEPRGVITYLIPSPDLXENGTPKLTCLVLDLSEENITVTWVRKKSIGAS 179
Db 121 KCADSNPRGSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHS 180
Qy 180 QRSTKHHTATSIILPVDADKWIEGEGYQCRVDHPFPKPIVRSITKLPGRLAPEV 239
Db 181 RKEKQRNGTITVTSTPLPVGTRDWIEGETYQCRVTHPLPALMRSTTKLPGRLAPEV 240
Qy 240 MLPPSPETGTRTTCCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPSPFL 299
Db 241 MLPPSPETGTRTTCCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPSPFL 300
Qy 300 YSRMLVNKSIWEKGNLTCRVVHEALPGSRTLKSLHYSAGN 341
Db 301 YSRMLVNKSIWEKGNLTCRVVHEALPGSRTLKSLHYSAGN 342
RESULT 5
AAB06202
ID AAB06202 standard; protein; 341 AA.
XX AC AAB06202;
XX AC AAB06202;
XX DT 22-NOV-2000 (first entry)
XX DE Immunogenic peptide consisting of opossum CH2, mouse CH3 and opossum CH4.
XX KW Mouse; opossum; immunoglobulin E; IGE; vaccination; infection; allergy;
XX KW asthma; eczema; immunogenic peptide.
XX OS Chimeric - Didelphis virginiana.
XX OS Chimeric - Mus sp.
XX PN Key Location/Qualifiers
XX XX
XX FT Misc-difference 1.341
XX FT /label= OTHER
XX FT /note= "Xaa=unknown"
XX FT
XX XX
```

PN WO200025722-A2.
 XX 11-MAY-2000.
 XX 21-OCT-1999; 99WO-SE01896.
 XX 02-NOV-1998; 98US-0106652.
 PR 22-SEP-1999; 99US-0401636.
 XX (RESI-) RESISTENTIA PHARM AB.
 PA Hellman LT;
 XX WPI; 2000-365342/31.
 XX Immunogenic polypeptides useful for preventing the harmful effects of
 PT immunoglobulin E in mammals -
 XX Disclosure; Fig 2; 50pp; English.
 XX The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain
 CC constant region 3 from the mouse. It was shown to cause a stronger
 CC polyclonal anti-self IgE response than peptides consisting of the same
 CC regions from one mammal. Immunogenic peptides, particularly those
 CC consisting of different heavy chain constant regions, can be used for
 CC vaccination in humans, against bacterial and viral infections and
 CC allergies, such as asthma, fur, pollen and food allergies and eczema.
 XX Sequence 341 AA;

Query Match 82.8%; Score 1539; DB 21; Length 341;
 Best Local Similarity 85.9%; Pred. No. 1.7e-119;
 Matches 293; Conservative 12; Mismatches 34; Indels 2; Gaps 2;
 QY 1 EPHHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
 DB 1 EPHHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
 QY 61 LVDGQEAENLPFYTRPKREGGQTFSLQSEVNITQGMSSNTYTVCHVKHNGSIFEDSSR 120
 DB 61 LVDGQEAENLPFYTRPKREGGQTFSLQSEVNITQGMSSNTYTVCHVKHNGSIFEDSSR 120
 QY 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVTVRERKKSIGSASQ 180
 DB 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVTVRERKKSIGSASQ 180
 QY 181 RSTKHHAHTTITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVY 239
 DB 180 WYTKHHHAHTTITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVY 239
 QY 240 MLPSPPEETGTRTVTCLIRGYPSEISVQWLPNNNEEDHTGHTTTRPKDGTDPSPFL 299
 DB 240 MLPSPPEETGTRTVTCLIRGYPSEISVQWLPNNNEEDHTGHTTTRPKDGTDPSPFL 299
 QY 300 YSRMLVKSWEKGNLVTCRVVHEALPGSRTLEKSLHYSAG 340
 DB 300 YSRMLVKSWEKGNLVTCRVVHEALPGSRTLEKSLHYSAG 340

RESULT 6
 AAB03644
 ID AAB03644 standard; protein; 341 AA.
 AC AAB03644;
 XX 22-NOV-2000 (first entry)
 DE Opossum IgE heavy chain constant regions 2, 3 and 4.
 XX Opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
 KW asthma; eczema; immunogenic peptide.

OS Didelphis virginiana.
 XX WO200025722-A2.
 XX 11-MAY-2000.
 XX 21-OCT-1999; 99WO-SE01896.
 XX 02-NOV-1998; 98US-0106652.
 PR 22-SEP-1999; 99US-0401636.
 XX (RESI-) RESISTENTIA PHARM AB.
 PA Hellman LT;
 XX WPI; 2000-365342/31.
 XX Immunogenic polypeptides useful for preventing the harmful effects of
 PT immunoglobulin E in mammals -
 XX Disclosure; Fig 1; 50pp; English.
 XX The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2, 3 and 4 of the opossum IgE. It was used to
 CC construct a number of immunogenic peptides which consisted of regions of
 CC IgE from different mammals, which appear to cause a stronger polyclonal
 CC anti-self IgE response than peptides consisting of the same regions from
 CC one mammal. Immunogenic peptides, particularly those consisting of
 CC different heavy chain constant regions, can be used for vaccination
 CC in humans, against bacterial and viral infections and allergies, such
 CC as asthma, fur, pollen and food allergies and eczema.
 XX Sequence 341 AA;
 SQ Query Match 82.1%; Score 1526; DB 21; Length 341;
 Best Local Similarity 80.4%; Pred. No. 2e-118;
 Matches 274; Conservative 29; Mismatches 38; Indels 0; Gaps 0;
 QY 1 EPHHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
 DB 1 EPHHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
 QY 61 LVDGQEAENLPFYTRPKREGGQTFSLQSEVNITQGMSSNTYTVCHVKHNGSIFEDSSR 120
 DB 61 LVDGQEAENLPFYTRPKREGGQTFSLQSEVNITQGMSSNTYTVCHVKHNGSIFEDSSR 120
 QY 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVTVRERKKSIGSASQ 180
 DB 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVTVRERKKSIGSASQ 180
 QY 181 RSTKHHAHTTITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVY 240
 DB 181 VYKEQYNGTFTVTSHLPVNTDDWIEGDTYTCRLSPDMPVPLIRTISKAPGRKLAPEVY 240
 QY 241 LPPSPPEETGTRTVTCLIRGYPSEISVQWLPNNNEEDHTGHTTTRPKDGTDPSPFL 300
 DB 241 LPPSPPEETGTRTVTCLIRGYPSEISVQWLPNNNEEDHTGHTTTRPKDGTDPSPFL 300
 QY 301 SRMLVKSWEKGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
 DB 301 SRMLVKSWEKGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
 RESULT 7
 AAB06201
 ID AAB06201 standard; protein; 342 AA.
 AC AAB06201;
 XX 22-NOV-2000 (first entry)
 DE Immunogenic peptide consisting of opossum CH2, CH4 and rat/opossum CH3.
 XX

KW Rat; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
 XX asthma; eczema; immunogenic peptide.

OS Chimeric - Didelphis virginiana.
 OS Chimeric - Rattus sp.

XX Key Location/Qualifiers
 XX Misc-difference 1..342
 FT /label= OTHER
 FT /note= "Xaa=unknown"

PT WO200025722-A2.

XX 11-MAY-2000.

XX 21-OCT-1999; 99WO-SE01896.

XX 02-NOV-1998; 98US-0106652.

PR 22-SEP-1999; 99US-0401636.

XX (RESI-) RESISTENTIA PHARM AB.

XX Hellman LT;

XX WPI; 2000-365342/31.

XX Immunogenic polypeptides useful for preventing the harmful effects of
 PT immunoglobulin E in mammals -

XX Disclosure; Fig 2; 50pp; English.

CC The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain
 CC constant region 3 created from a combination of the one from the rat
 CC and the one from the opossum. It was shown to cause a stronger
 CC polyclonal anti-self IgE response than peptides consisting of the same
 CC regions from one mammal. Immunogenic peptides, particularly those
 CC consisting of different heavy chain constant regions, can be used for
 CC vaccination in humans, against bacterial and viral infections and
 CC allergies, such as asthma, fur, pollen and food allergies and eczema.

XX Sequence 342 AA;

Query Match 81.4%; Score 1511.5; DB 21; Length 342;

Best Local Similarity 83.6%; Pred. No. 3.2e-117;

Matches 285; Conservative 16; Mismatches 39; Indels 1; Gaps 1;

Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTTM 60

Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTTM 60

Qy 61 LVDGQAEALFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKNGSIPEDSSR 120

Db 61 LVDGQAEALFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKNGSIPEDSSR 120

Qy 121 RCDDEPRGVITYLIPSPDLVNGTPKLCLVLDLESEENITVTVWRKKISGTSASQ 180

Db 121 RCDDEPRGVITYLIPSPDLVNGTPKLCLVLDLESEENITVTVWRKKISGTSASQ 180

Qy 181 RSTKH-HHATTSITSLIPVDKADWIEGEGYQCRVDHPFPKPIVRSITKLPKRLAPVY 239

Db 181 LVVKEHYHGTFTXSHLPEVDDWIEGTYTXLSESPMIVILPTISALPKRLAPVY 240

Qy 240 MLPPSPETGTRITVTLIRGFPEISVQWLPNNEEDHTGHTTTRQKHGTDPSFFL 299

Db 241 MLPPSPETGTRITVTLIRGFPEISVQWLPNNEEDHTGHTTTRQKHGTDPSFFL 300

Qy 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLKSLHYSAG 340

Db 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLKSLHYSAG 341

RESULT 8

AAB03643

ID AAB03643 standard; protein; 340 AA.

XX AAB03643;

XX 22-NOV-2000 (first entry)

DE Rat IgE heavy chain constant regions 2, 3 and 4.

XX Rat; immunoglobulin E; IgE; vaccination; infection; allergy;
 XX asthma; eczema; immunogenic peptide.

OS Rattus sp.

XX WO200025722-A2.

XX 11-MAY-2000.

XX 21-OCT-1999; 99WO-SE01896.

XX 02-NOV-1998; 98US-0106652.

PR 22-SEP-1999; 99US-0401636.

XX (RESI-) RESISTENTIA PHARM AB.

XX Hellman LT;

XX WPI; 2000-365342/31.

XX Immunogenic polypeptides useful for preventing the harmful effects of
 PT immunoglobulin E in mammals -

XX Disclosure; Fig 1; 50pp; English.

CC The present sequence is an immunogenic peptide consisting of the
 CC heavy chain constant regions 2, 3 and 4 of the rat IgE. It was used to
 CC construct a number of immunogenic peptides which consisted of regions of
 CC IgE from different mammals, which appear to cause a stronger polyclonal
 CC anti-self IgE response than peptides consisting of the same regions from
 CC one mammal. Immunogenic peptides, particularly those consisting of
 CC different heavy chain constant regions, can be used for vaccination
 CC in humans, against bacterial and viral infections and allergies, such
 CC as asthma, fur, pollen and food allergies and eczema.

XX Sequence 340 AA;

Query Match 56.6%; Score 1051; DB 21; Length 340;

Best Local Similarity 62.6%; Pred. No. 5.2e-79;

Matches 206; Conservative 35; Mismatches 78; Indels 10; Gaps 3;

Qy 17 PVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTTMVDGQAEALFPYTTTR 76

Db 8 PVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTTMVDGQAEALFPYTTTR 76

Qy 77 PK----REGGQTFSLQSEVNITQGMSSNTYTCHVKNGSIPEDSSRCDDEPRGVIT 132

Db 62 AQNVLIKEEGKLASTYSLRNITQQWMSESTFTCKVTSQGENYWAHTRCSDDEPRGVIT 121

Qy 133 YLIPSPDLVNGTPKLCLVLDLESEENITVTVWRKKISGTSASORSTKHHHTTSI 192

Db 122 YLIPSPDLVNGTPKLCLVLDLESEENITVTVWRKKISGTSASORSTKHHHTTSI 181

Qy 193 TSILPVDKADWIEGEGYQCRVDHPFPKPIVRSITKLPKRLAPEVYMLPPSPETGTR 252

Db 182 TSILPVDKADWIEGEGYQCRVDHPFPKPIVRSITKLPKRLAPEVYMLPPSPETGTR 241

Qy 253 TVTCLIRGFPEISVQWLPNNEEDHTGHTTTRQKHGTDPSFFLYSRMLVNKSIWEK 312

Db 242 TLTLCLIQNFPEIDISVQWLDQSLPKQSHSTTTLKYNQSGNQRFPIFSRLEVTKALWTQ 301

Qy 313 GNLVTCRVVHEALPGSRTLKSLHYSAGN 341

Db 302 TKQFTCRVHEALREPRKRLERTISKSLGN 330

Qy 61 LVDQAEANLPPYTRPRKREGQTFSLQSEVNITQGMSSNTYTVCHVKH--NGSIFPDS 118
 Db 60 LVDGQKAHLFPYAPPREGNSFSHSEVHIITODWLSGKTFCTQVTVXLADKKTYQDS 119
 Qy 119 SRRCSDDPRGVITVLIIPSPDLVYENGTPKLTCLVLVLESEENITVTVRERKKSIGA 178
 Db 120 ARKADSDPRGITVFLTPSPDLVYISKTPKLTCLVLESEENITVTVRERKKSIGA 179
 Qy 179 SORSTKHHHATTSITSLPVDKAWIEGEGYQCRVDHPFPKPIVRSITKLPKRLAPEV 238
 Db 180 SFEKGKFXGTMFTISTVPAIQDNWEGESYTCXXAHPDLISPIIKTVTKLPKRLAPXV 239
 Qy 239 YMLPPSPETG--TTRVTCLIRGYPSEISVQWLPNNEEDHTGHHHTTRPKQKHGTDP 296
 Db 240 YAFPPHQAQEVSHXASLSLTCLIRGYPENISVRWLLDXKPLPTEHYRTTKPLKQGPDXA 299
 Qy 297 FFYSRLMVLNKSIVKGNLVCVVHVALPGSRITLKSLSHSAG 340
 Db 300 YFLYSRLAVHKSWEQGHVYTCVVHVALP-SRNTERKFQHTSG 342

RESULT 11
 AAU80300
 ID AAU80300 standard; Protein; 421 AA.
 AC AAU80300;
 XX
 XX
 DT 30-JUL-2002 (first entry)
 DE Mouse IgE heavy chain C1-C2-C3-C4 domains.
 KW IgE; allergy; mouse; antiallergic; immunosuppressive; antianaphylactic;
 KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
 KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
 KW heavy chain C domain.
 XX
 OS Mus sp.
 XX
 XX WO200220038-A2.
 XX
 XX 14-MAR-2002.
 XX
 XX 06-SEP-2001; 2001WO-DK00579.
 XX
 XX 06-SEP-2000; 2000DK-0001326.
 PR
 PR 15-SEP-2000; 2000US-232831P.
 XX
 PA (PHAR-) PHARMEXA AS.
 XX
 XX Klysner S, Von Hoegen P, Voldborg B, Gautam A;
 XX
 XX WPI; 2002-383033/41.
 XX
 XX Inducing immune response against autologous immunoglobulin E in an
 PT animal, by effecting simultaneous presentation of cytotoxic T
 PT lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
 PT -
 XX
 PS Examples; Page 145-147; 151pp; English.
 XX
 XX This invention relates to a novel method for inducing an immune response
 CC against autologous immunoglobulin E (IgE) in an animal. The method
 CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
 CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell
 CC epitope (TH epitope) which is foreign to the animal, by antigen
 CC presenting cells (APCs) of the animal's immune system. The epitopes
 CC of the invention may be used as a vaccine against allergic diseases. The
 CC method of the invention is useful for inducing an immune response
 CC against autologous IgE in an animal, which is useful for downregulating
 CC autologous IgE in the animal. This method is useful in the prevention
 CC and treatment of allergic diseases such as anaphylaxis, allergic
 CC rhinitis, asthma and atopic dermatitis. The present sequence represents

CC the mouse IgE heavy chain C1-C2-C3-C4 domains used to create the
 CC epitopes of the invention.

SQ Sequence 421 AA;

Query Match 50.6%; Score 940.5; DB 23; Length 421;
 Best Local Similarity 55.2%; Pred. No. 1e-69;

Matches 191; Conservative 46; Mismatches 100; Indels 9; Gaps 5;

Qy 2 FHHHHHTLSLPES-----GFTVTIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPARV 56

Db 73 FTCHVTHPPSPFNSERTILVRFPVNITEPTLELLHSSCDPNA-FHSTIQLCYFIYGHILNDV 131

Qy 57 HVTWLVDCQAEANLFPYTRPRKREGQTFSLQSEVNITQGMSSNTYTVCHVKHNGSIFE 116

Db 132 SVSWMDDREITDITLAQTVLKEE-GKLASTCSKLNITEQQMSESTFTCKVTSQGVLYL 190

Qy 117 DSSRRCSDDPRGVITVLIIPSPDLVYENGTPKLTCLVLVLESEENITVTVRERKKSIG 176

Db 191 AHTRRCPDHPRGVITVLIIPSPDLVYQNGAPKLTCLVVDLESEKKNVNTWNEKKTIV- 249

Qy 177 SASORSTKHH-HATTSITSLPVDKAWIEGEGYQCRVDHPFPKPIVRSITKLPKRLA 235

Db 250 SASQWYTKHNNATTSITSLPVDKAWIEGEGYQCIVDHPDFPKPIVRSITKTFQRSA 309

Qy 236 PEVYMLPPSPETGTTTRVTCLIRGYPSEISVQWLPNNEEDHTGHHHTTRPKQKHGTDP 295

Db 310 PEVYVFPPEESEDKRTLCTLIQNFPEDISVQWLGDKLISNSOHSSTTTPLKNGSNQ 369

Qy 296 SFFLYSRLMVLNKSIVKGNLVCVVHVALPGSRITLKSLSHSAGN 341

Db 370 GFFIFSRLEVAKTLMTQRKQFTQCVIHEALQKPKLEKTISTSLGN 415

RESULT 12

AAU80300
 ID AAR97753 standard; Protein; 426 AA.

AC AAR97753;
 XX
 XX
 DT 28-AUG-1996 (first entry)
 DE
 DE Canine IgE.
 XX
 XX IgE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
 XX
 XX Canis familiaris.
 XX
 XX WO9614867-A1.
 XX
 XX 23-MAY-1996.
 XX
 XX 03-NOV-1995; 95WO-US13795.
 XX
 XX 09-NOV-1994; 94US-0336891.
 PR
 PR 09-NOV-1994; 94US-0336583.
 XX
 XX (MERI) MERCK & CO INC.
 XX
 XX Hollis GF, Patel MD;
 XX
 XX WPI; 1996-277321/28.
 DR
 DR N-PSDB; AAT29824.
 XX
 XX New DNA encoding canine IgE and IgA - useful in vaccines, antisense
 PT therapy, assays, drug screening, etc.
 PT
 XX Claim 11; Page 29-30; 49pp; English.
 XX
 XX The canine IgE amino acid sequence (AAR97753) was deduced from
 CC an isolated gene (AAT29824) obtd. from a canine liver DNA library.
 CC The cloning of the IgE gene allows prodn. of large quantities of
 CC recombinant IgE using bacterial, yeast, mammalian, insect or

CC vital systems. The IgE can be used in drug development (e.g.
 CC small molecule screening, assay development and anti-IgE
 CC antibody generation). Fragments of IgE can be used in vaccines
 CC or to prevent IgE-mediated hypersensitivity. The new sequence
 CC information permits targeted modulation of IgE-mediated immune
 CC responses.

XX Sequence 426 AA;

Query Match 50.5%; Score 938.5; DB 17; Length 426;
 Best Local Similarity 53.2%; Pred. No. 1.5e-69;
 Matches 173; Conservative 53; Mismatches 96; Indels 3; Gaps 2;

Qy 18 VTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDGQAEANLPYITRP 77
 Db 102 LNFIPPTVKLFHSSCNPGVDHTTIIQLCLISGYVPGDMEVILVDGQKATNIFYPTAGP 161
 Qy 78 KREGGOTFSLOEAVNITQGWMSNTYTCHVKHNGSIFEDSSRRCSDDPRGVITLIPP 137
 Db 162 TKEGNTV-STHSEINITQGEWSQKTYTCQVYQFTFKDEARKSESDPRGVITLIPP 220
 Qy 138 SPLDYENGTPKLTCLVLDLESEENITVWVRERKKSIGASQSRSTKHHTTSITSLP 197
 Db 221 SPLDYVHKAPKITCLVLDLATWEGNLTWYRESKEPVNPGPLNKKDFNGITITVTSTLP 280
 Qy 198 VDADKWIIEGEGYQCRVDHHPFKPIVRSITKLPKGLAPEVYMLPPSPETGTR--TVT 255
 Db 281 VNTNDWIEGETYICRVTHPLPKDIVRSIAKAPGRAPDVYLFPPPEQQGTQKRVTLT 340
 Qy 256 CLIRGFYSEISVQWLPNNEEDHTGHTTTRPKDGHGTDPSFFLYSRMLVNSIWEKGNL 315
 Db 341 CLIQNFFADISVQWLRNDSPTQDTQYTTGPHKVGSRPAFFISRLVSRVDNEQKX 400
 Qy 316 VTCRVVHEALPGSRITLKSLSHYSAG 340
 Db 401 FTCQVHEALSGSRILQKWSKTPG 425

RESULT 13

AAU80297

ID AAU80297 standard; Protein; 332 AA.

XX AC AAU80297;

XX DT 30-JUL-2002 (first entry)

XX DE Mouse IgE heavy chain C2-C3-C4 domain with MIGIS fragment.

XX KW IgE; allergy; mouse; antiallergic; immunosuppressive; antianaphylactic;

XX KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;

XX KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;

XX KW heavy chain C domain; MIGIS.

XX OS Mus sp.

XX OS Synthetic.

XX XX WO200220038-A2.

XX PD 14-MAR-2002.

XX PF 06-SEP-2001; 2001WO-DK00579.

XX XX 06-SEP-2000; 2000DK-0001326.

PR 15-SEP-2000; 2000US-232831P.

XX XX (PHAR-) PHARMEXA AS.

XX PI Klysner S, Von Hoegen P, Voldborg B, Gautam A;

XX XX WPI; 2002-383033/41.

XX DR Inducing immune response against autologous immunoglobulin E in an

PT animal, by effecting simultaneous presentation of cytotoxic T

PT animal.

PT lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
 PT Examples; Page 137-138; 151pp; English.

XX This invention relates to a novel method for inducing an immune response
 CC against autologous immunoglobulin E (IgE) in an animal. The method
 CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
 CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell
 CC epitope (TH epitope) which is foreign to the animal, by antigen
 CC presenting cells (APCs) of the animal's immune system. The epitopes
 CC of the invention may be used as a vaccine against allergic diseases. The
 CC method of the invention is useful for inducing an immune response
 CC against autologous IgE in an animal, which is useful for downregulating
 CC autologous IgE in the animal. This method is useful in the prevention
 CC and treatment of allergic diseases such as anaphylaxis, allergic
 CC rhinitis, asthma and atopic dermatitis. The present sequence represents
 CC the mouse IgE heavy chain C2-C3-C4 domain with the MIGIS fragment used
 CC to create the epitopes used in the method of the invention.

XX Sequence 332 AA;

Query Match 50.4%; Score 936; DB 23; Length 332;
 Best Local Similarity 56.7%; Pred. No. 1.8e-69;
 Matches 185; Conservative 46; Mismatches 91; Indels 4; Gaps 4;

Qy 17 PVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDGQAEANLPYITRP 76
 Db 4 PVNITEPTLELLHSSCDPNA-FHSTIQLYCFYGHILNDVSVSLMDREITDTLTAQTVL 62
 Qy 77 PKREGGOTFSLOEAVNITQGWMSNTYTCHVKHNGSIFEDSSRRCSDDPRGVITLIPP 136
 Db 63 IKEE-GKLAUASCUNITEQMMSESTFTCKVTSOGVDYLAHRCPPDHPKGVITYLIP 121
 Qy 137 PSLDYENGTPKLTCLVLDLESEENITVWVRERKKSIGASQSRSTKH-HATTSITSI 195
 Db 122 PSLDYQNGAPKLTCLVLDLESEKVNVTWNQEKTSV-SASQWYTKHNNATTSITSI 180
 Qy 196 LPVADKWIIEGEGYQCRVDHHPFKPIVRSITKLPKGLAPEVYMLPPSPETGTRTVT 255
 Db 181 LPVADKWIIEGEGYQCIVDHDPFKPIVRSITKTPQRSAPVYVFPPEESEDKRTLT 240
 Qy 256 CLIRGFYSEISVQWLPNNEEDHTGHTTTRPKDGHGTDPSFFLYSRMLVNSIWEKGNL 315
 Db 241 CLIQNFFADISVQWLRNDSPTQDTQYTTGPHKVGSRPAFFISRLVSRVAKTLTQKQ 300
 Qy 316 VTCRVVHEALPGSRITLKSLSHYSAGN 341
 Db 301 FTCQVHEALQKPKLEXTISTSLGN 326

RESULT 14

AAU80298

ID AAU80298 standard; Protein; 332 AA.

XX AC AAU80298;

XX XX 30-JUL-2002 (first entry)

XX DE Murine IgE heavy chain C2-C3-C4 for mammalian expression.

XX KW IgE; allergy; mouse; antiallergic; immunosuppressive; antianaphylactic;

XX KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;

XX KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;

XX KW heavy chain C domain.

XX OS Mus sp.

XX OS Synthetic.

XX XX WO200220038-A2.

XX PD 14-MAR-2002.

PF 06-SEP-2001; 2001WO-DK00579.
XX
XX DE
XX PR 06-SEP-2000; 2000DK-0001326.
XX PR 15-SEP-2000; 2000US-232831P.
XX PA (PHAR-) PHARMEXA AS.
XX
XX PI Klysner S, Von Hoegen P, Voldborg B, Gautam A;
XX DR WPI; 2002-383033/41.
XX DR N-PSDB; ABK51142.
XX
XX PT Inducing immune response against autologous immunoglobulin E in an
XX PT animal, by effecting simultaneous presentation of cytotoxic T
XX PT lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
XX
XX PS Disclosure; Page 140-141; 151pp; English.
XX
XX CC This invention relates to a novel method for inducing an immune response
XX CC against autologous immunoglobulin E (IGE) in an animal. The method
XX CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
XX CC (CTL) epitope and/or B-cell epitope derived from IGE, and T helper cell
XX CC epitope (TH epitope) which is foreign to the animal, by antigen
XX CC presenting cells (APCs) of the animal's immune system. The epitopes
XX CC of the invention may be used as a vaccine against allergic diseases. The
XX CC method of the invention is useful for inducing an immune response
XX CC against autologous IGE in an animal, which is useful for downregulating
XX CC autologous IGE in the animal. This method is useful in the prevention
XX CC and treatment of allergic diseases such as anaphylaxis, allergic
XX CC rhinitis, asthma and atopic dermatitis. The present sequence represents
XX CC the mouse IGE heavy chain C2-C3-C4 domain optimised for a mammalian
XX CC expression system used to create the epitopes used in the method of the
XX CC invention.
XX SQ Sequence 332 AA;

Query Match 50.4%; Score 936; DB 23; Length 332;
Best Local Similarity 56.7%; Pred. No. 1.8e-69;
Matches 185; Conservative 46; Mismatches 91; Indels 4; Gaps 4;

QY 17 PVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTVLWDQGEAENLPFYTR 76
Db 4 PWNITEPTLELLHSSCDPNA-FHSTIQLYCFIYGHILNDVSVSLMDDREITDTLAQTVL 62

QY 77 PKREGGQTFSLQSEVNITQGWMSNTYTCVKHNGSIFEDSSRRCSDEPRGVITYLIP 136
Db 63 IKEE-GKLASTCSKLNITEQWMSSEFTCKVTSQGVYLAHTRCPDHPRGVITYLIP 121

QY 137 PSLDLYENGTPKLTCLVLDLESENIYVTVWRERKKSIGSASQSRSTKH-HATTSTSI 195
Db 122 PSLDLYQNGAPKLTCLVLDLESEKNVNTWNOEKKTSV-SASQWYTKHNNATTSITS 180

QY 196 LPVDAKWIEGEGYQCRVDHPFKPIVRSITKLPGRKLAPEVYMLPPSPETGTRTVT 255
Db 181 LPVAKWIEGYGQICVDHPDFPKPIVRSITKTPGQSAPEVYVFPPESEEDKRTL 240

QY 256 CLIRGFYPSISVQWLPNNEEDHTGHHHTTRPKQDHGTDPSFFLYSRMLVNKSIWEKGNL 315
Db 241 CLIQNFEDISVQWLGKGLINSQHSITTPKSGNSQGFIFSRLEVAKLWTQRQ 300

QY 316 VTCRVVHEALPGSRFTLEKSLHYSAGN 341
Db 301 FTCQVTHEALQPKRLEKTIISTISLGN 326

RESULT 15
AAU80299
ID AAU80299 standard; Protein; 332 AA.
XX
XX AC AAU80299;
XX DT 30-JUL-2002 (first entry)

XX Murine IGE heavy chain C2-C3-C4 for E.Coli expression.
XX DE
XX KW IGE; allergic; mouse; antiallergic; immunosuppressive; antianaphylactic;
XX KW antiaachmatic; dermatological; antiinflammatory; immunoglobulin E; IGE;
XX KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
XX KW heavy chain C domain.
XX OS Mus sp.
XX OS Synthetic.
XX PN W0200220038-A2.
XX PD 14-MAR-2002.
XX PF 06-SEP-2001; 2001WO-DK00579.
XX PR 06-SEP-2000; 2000DK-0001326.
XX PR 15-SEP-2000; 2000US-232831P.
XX PA (PHAR-) PHARMEXA AS.
XX PI Klysner S, Von Hoegen P, Voldborg B, Gautam A;
XX XX WPI; 2002-383033/41.
XX DR N-PSDB; ABK51142.
XX
XX PT Inducing immune response against autologous immunoglobulin E in an
XX PT animal, by effecting simultaneous presentation of cytotoxic T
XX PT lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
XX
XX PS Disclosure; Page 144-145; 151pp; English.
XX
XX CC This invention relates to a novel method for inducing an immune response
XX CC against autologous immunoglobulin E (IGE) in an animal. The method
XX CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
XX CC (CTL) epitope and/or B-cell epitope derived from IGE, and T helper cell
XX CC epitope (TH epitope) which is foreign to the animal, by antigen
XX CC presenting cells (APCs) of the animal's immune system. The epitopes
XX CC of the invention may be used as a vaccine against allergic diseases. The
XX CC method of the invention is useful for inducing an immune response
XX CC against autologous IGE in an animal, which is useful for downregulating
XX CC autologous IGE in the animal. This method is useful in the prevention
XX CC and treatment of allergic diseases such as anaphylaxis, allergic
XX CC rhinitis, asthma and atopic dermatitis. The present sequence represents
XX CC the mouse IGE heavy chain C2-C3-C4 domain optimised for an E.Coli
XX CC expression system used to create the epitopes used in the method of the
XX CC invention.
XX SQ Sequence 332 AA;

Query Match 50.4%; Score 936; DB 23; Length 332;
Best Local Similarity 56.7%; Pred. No. 1.8e-69;
Matches 185; Conservative 46; Mismatches 91; Indels 4; Gaps 4;

QY 17 PVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTVLWDQGEAENLPFYTR 76
Db 4 PWNITEPTLELLHSSCDPNA-FHSTIQLYCFIYGHILNDVSVSLMDDREITDTLAQTVL 62

QY 77 PKREGGQTFSLQSEVNITQGWMSNTYTCVKHNGSIFEDSSRRCSDEPRGVITYLIP 136
Db 63 IKEE-GKLASTCSKLNITEQWMSSEFTCKVTSQGVYLAHTRCPDHPRGVITYLIP 121

QY 137 PSLDLYENGTPKLTCLVLDLESENIYVTVWRERKKSIGSASQSRSTKH-HATTSTSI 195
Db 122 PSLDLYQNGAPKLTCLVLDLESEKNVNTWNOEKKTSV-SASQWYTKHNNATTSITS 180

QY 196 LPVDAKWIEGEGYQCRVDHPFKPIVRSITKLPGRKLAPEVYMLPPSPETGTRTVT 255
Db 181 LPVAKWIEGYGQICVDHPDFPKPIVRSITKTPGQSAPEVYVFPPESEEDKRTL 240

QY 256 CLIRGFYPSISVQWLPNNEEDHTGHHHTTRPKQDHGTDPSFFLYSRMLVNKSIWEKGNL 315

Db 241 CLIQFFPDISVQWLGDKLISNSQHSSTTTPKSGNSQGFIESRLEVAKTLWTQRKQ 300
Qy 316 VTCRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 FTCQVIHEALQKPRKLEKTISTSLGN 326

Search completed: March 8, 2003, 07:48:13
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: March 8, 2003, 07:46:20 ; Search time 33 Seconds
(without alignments)
2129.154 Million cell updates/sec

Title: US-09-401-636-4
Perfect score: 1858
Sequence: 1 EFRHHHHTLSLPESGPVTI.....HEALPGSRTLEKSLHYSAGN 341

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : SPTREMBL 21:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	488.5	26.3	375	4 Q9BSZ1	Q9bsz1 homo sapien
2	488.5	26.3	588	4 Q8WUX4	Q8wux4 homo sapien
3	488.5	26.3	597	4 Q9BQ88	Q9bqb8 homo sapien
4	488.5	26.3	597	4 Q96BB9	Q96bb9 homo sapien
5	488.5	26.3	597	4 Q9BU10	Q9bul10 homo sapien
6	488.5	26.3	613	4 Q96EY0	Q96ey0 homo sapien
7	488.5	26.3	613	4 Q8WUK1	Q8wuk1 homo sapien
8	488.5	26.3	614	4 Q96GK6	Q96gak6 homo sapien
9	488.5	26.3	618	4 Q96AA6	Q96aa6 homo sapien
10	463	24.9	337	6 Q95M34	Q95m34 equus caball
11	455.5	24.5	613	11 Q8VCX7	Q8vcx7 mus musculus
12	455	24.5	473	4 Q8TC63	Q8tc63 homo sapien
13	441.5	23.8	471	4 Q8TC77	Q8tc77 homo sapien
14	435	23.4	437	11 Q9RIA4	Q9ria4 mus musculus
15	434.5	23.4	463	11 Q99IC4	Q99ic4 mus musculus
16	429.5	23.1	469	11 Q8R3V9	Q8r3v9 mus musculus

17	424.5	22.8	473	11 Q9DBL4	Q9dbl4 mus musculus
18	406	21.9	473	11 Q91Z05	Q91z05 mus musculus
19	406	21.9	474	11 Q8R3H6	Q8r3h6 mus musculus
20	400.5	21.6	468	11 Q99L31	Q99l31 mus musculus
21	400.5	21.6	473	11 Q99L25	Q99l25 mus musculus
22	390	21.0	701	4 Q96BQ8	Q96bq8 homo sapien
23	355	19.1	416	4 Q9NPP6	Q9npp6 homo sapien
24	347.5	18.7	384	4 Q9UP60	Q9up60 homo sapien
25	346.5	18.6	494	4 Q96K68	Q96k68 homo sapien
26	346.5	18.6	496	4 Q96KX8	Q96kx8 homo sapien
27	345.5	18.6	496	4 Q96DK0	Q96dk0 homo sapien
28	344.5	18.5	497	4 Q8WY24	Q8wy24 homo sapien
29	336.5	18.1	500	4 Q9BRV0	Q9brv0 homo sapien
30	333.5	17.9	426	11 Q9DCD9	Q9dcd9 mus musculus
31	330.5	17.8	486	11 Q91Z07	Q91z07 mus musculus
32	330.5	17.8	487	11 Q99KA4	Q99ka4 mus musculus
33	326	17.5	479	11 Q99M22	Q99m22 mus musculus
34	326	17.5	481	11 Q8VCV5	Q8vcv5 mus musculus
35	326	17.5	484	11 Q99LA6	Q99la6 mus musculus
36	322.5	17.4	684	13 Q90544	Q90544 ginglymoeto
37	314	16.9	488	11 Q91WR1	Q91wr1 mus musculus
38	314	16.9	489	11 Q8VCX4	Q8vcx4 mus musculus
39	313	16.8	481	11 Q91WT3	Q91wt3 mus musculus
40	313	16.8	481	11 Q91WT1	Q91wt1 mus musculus
41	313	16.8	482	11 Q91X92	Q91x92 mus musculus
42	313	16.8	484	11 Q8VEA0	Q8vea0 mus musculus
43	312	16.8	480	11 Q91XE1	Q91xe1 mus musculus
44	311	16.7	479	11 Q91WP5	Q91wp5 mus musculus
45	210	11.3	573	4 Q8WU38	Q8wu38 homo sapien

ALIGNMENTS

RESULT 1

Q9BSZ1	ID	Q9BSZ1	PRELIMINARY;	PRT;	375 AA.
AC	Q9BSZ1;				
DT	01-JUN-2001	(TrEMBLrel. 17, Created)			
DT	01-JUN-2001	(TrEMBLrel. 17, Last sequence update)			
DT	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)			
DE	Hypothetical 41.3 Kda protein.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=LYMPH;				
RA	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.				
RL	EMBL; BC004476; AAH04476.1; -				
DR	HSSP; P01857; IFC1.				
DR	InterPro; IPR003597; Ig_cl.				
DR	InterPro; IPR003600; Ig_like.				
DR	Pfam; PF00047; Ig_3.				
DR	SMART; SM00407; IGcl; 3.				
DR	SMART; SM00410; IG_like; 1.				
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_3.				
KW	Hypothetical protein.				
SQ	SEQUENCE 375 AA; 41314 MW; B1A0A0998F473619 CRC64;				

Query Match 26.3%; Score 488.5; DB 4; Length 375;

Best Local Similarity 31.2%; Pred.No. 2.2e-37; Matches 105; Conservative 73; Mismatches 134; Indels 25; Gaps 10;

Qy 17 PVTII---PPVTKLFFHSSCDPR---GDAHSTIQLLCVSGFSAPKAVHTVLVDQEAEN 69

Db 24 PLPIVAELPPKVSVF---VPRDGFEGNPKRS-KLICATGFSRQIQVSMLEKQVGS 79

Qy 70 LFPVTT-----RPKREGQQTFSLOSSEVNTYTCQWMSNTYTCYKHKNGSIF-EQSSRRCS 123

```
Db 80 --GVTTDQVQAEAKESGPTTYKVTSTLTITIKESDWLSQSMTFCRVDRHGLTFOQNASSMCV 137
Qy 124 DDEPRGVITYLIPSPDLIDYENGTKLCLCLDLSEENITVTVRERKKSIGSASQST 183
Db 138 PQDQTAIRFAIPSPFASIFLTKSLKTLCLVTLDTLTSVTSWTRQNGEAVKHTNISE 197
Qy 184 KHHATTSTISILPVDAKDWIEGEGYQCRVDHPHPPKPIVRISITKLPKRL-APEVYMLP 242
Db 198 SHPNATFSAVGEASICEDDWSNGERFTCTVTHDLPSPKQTIISRPKGVALLHRPDIYLLP 257
Qy 243 PSPEETG--TTRTVTLIRGYPSEISVQWLPNNBEDHTGHHTTTRPKQDGHGTDPSPFLY 300
Db 258 PAREQLNLRRESATITCLVTGFSADVFVQWMQOGPLSPEKYVTSAPMPEQAPGRYFAH 317
Qy 301 SRMLVNSIWEKGNLVTCTRVVHEALPG---SRTLEKS 334
Db 318 SILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKS 354
```

RESULT 2

```
Q8WUX4 PRELIMINARY; PRT; 588 AA.
AC Q8WUX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 64.4 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAUSBERG R.;
RC TISSUE=LYMPH;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_5.
DR SMART; SM00409; Ig_2.
DR SMART; SM00407; Ig_c1.
DR SMART; SM00406; Ig_v.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;
```

```
Query Match 26.3%; Score 488.5; DB 4; Length 588;
Best Local Similarity 31.2%; Pred. No. 4.1e-37;
Matches 105; Conservative 73; Mismatches 134; Indels 25; Gaps 10;

Qy 17 PVTII---PPTVKLFHSSCDPR---GDAHSTIQLCLVSGFSPAKVHVTVLWDGQAEAN 69
Db 246 PLPVIAELPPKVSVP---VPPRDGFFGNPKS-KLICQATGFSRQIQVSWLREGKQVGS 301
Qy 70 LPFYTT-----RPKREGGQTFSLQSEVNITQGMSSNTYTCVHKVNGSIP-EDSSRRCS 123
Db 302 --GVTTDQVQAEAKESGPTTYKVTSTLTITIKESDWLSQSMTFCRVDRHGLTFOQNASSMCV 359
Qy 124 DDEPRGVITYLIPSPDLIDYENGTKLCLCLDLSEENITVTVRERKKSIGSASQST 183
Db 360 PQDQTAIRFAIPSPFASIFLTKSLKTLCLVTLDTLTSVTSWTRQNGEAVKHTNISE 419
Qy 184 KHHATTSTISILPVDAKDWIEGEGYQCRVDHPHPPKPIVRISITKLPKRL-APEVYMLP 242
Db 420 SHPNATFSAVGEASICEDDWSNGERFTCTVTHDLPSPKQTIISRPKGVALLHRPDIYLLP 479
Qy 243 PSPEETG--TTRTVTLIRGYPSEISVQWLPNNBEDHTGHHTTTRPKQDGHGTDPSPFLY 300
Db 480 PAREQLNLRRESATITCLVTGFSADVFVQWMQOGPLSPEKYVTSAPMPEQAPGRYFAH 539
```

```
Qy 301 SRMLVNSIWEKGNLVTCTRVVHEALPG---SRTLEKS 334
Db 540 SILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKS 576

RESULT 3
Q9BOB8 PRELIMINARY; PRT; 597 AA.
AC Q9BOB8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Unknown (protein for MGC:1905) (protein for MGC:1228).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAUSBERG R.;
RC TISSUE=MUSCLE;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -.
DR EMBL; BC001872; AAH01872.1; -.
DR HSSP; P01825; 7PAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_5.
DR SMART; SM00409; Ig_2.
DR SMART; SM00407; Ig_c1.
DR SMART; SM00406; Ig_v.
DR SMART; SM00410; Ig_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 26.3%; Score 488.5; DB 4; Length 597;
Best Local Similarity 31.2%; Pred. No. 4.2e-37;
Matches 105; Conservative 73; Mismatches 134; Indels 25; Gaps 10;

Qy 17 PVTII---PPTVKLFHSSCDPR---GDAHSTIQLCLVSGFSPAKVHVTVLWDGQAEAN 69
Db 246 PLPVIAELPPKVSVP---VPPRDGFFGNPKS-KLICQATGFSRQIQVSWLREGKQVGS 301
Qy 70 LPFYTT-----RPKREGGQTFSLQSEVNITQGMSSNTYTCVHKVNGSIP-EDSSRRCS 123
Db 302 --GVTTDQVQAEAKESGPTTYKVTSTLTITIKESDWLSQSMTFCRVDRHGLTFOQNASSMCV 359
Qy 124 DDEPRGVITYLIPSPDLIDYENGTKLCLCLDLSEENITVTVRERKKSIGSASQST 183
Db 360 PQDQTAIRFAIPSPFASIFLTKSLKTLCLVTLDTLTSVTSWTRQNGEAVKHTNISE 419
Qy 184 KHHATTSTISILPVDAKDWIEGEGYQCRVDHPHPPKPIVRISITKLPKRL-APEVYMLP 242
Db 420 SHPNATFSAVGEASICEDDWSNGERFTCTVTHDLPSPKQTIISRPKGVALLHRPDIYLLP 479
Qy 243 PSPEETG--TTRTVTLIRGYPSEISVQWLPNNBEDHTGHHTTTRPKQDGHGTDPSPFLY 300
Db 480 PAREQLNLRRESATITCLVTGFSADVFVQWMQOGPLSPEKYVTSAPMPEQAPGRYFAH 539

Qy 301 SRMLVNSIWEKGNLVTCTRVVHEALPG---SRTLEKS 334
Db 540 SILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKS 576

RESULT 4
```



```
Db 241 PLPVIAELPPKVSVF---VPPRDGFGNPKRS-KLICQATGFSPPQIQVSWLREGKQVGS 296
Qy 70 LFPYTT-----RPKREGGQTFSLQSEVNITQGWMSNTYTHVHNGSIP-EDSSRCS 123
Db 297 --GVTTDQVQAEAKESGPTTYKVTSLTIKESDWLSQSMFTCRVDHRLGTLTFOQNASSMCV 354
Qy 124 DDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVTVWRERKKSIGSASQST 183
Db 355 PQDQTAIRVFAIPSPFASIFLTSTLIKESDWLSQSMFTCRVDHRLGTLTFOQNASSMCV 414
Qy 184 KHHATTTSITSLPVDKADWIEGEGYQCRVDHPHPPKPIVRSITKLPGRKL-APEVYMLP 242
Db 415 SHPNATFSVAVGEASICEDDWNNGERFTCTVTHDLPSPKQTIISRPKGVALHRPDVYLLP 474
Qy 243 PSPETG---TTRTVCILRGFVPSISVQWLNNEDHTGHTTTRPKQKHGTDPSFFLY 300
Db 475 PAREQLNRESATITCLVTGFSFADVFVQWQMGQPLSPEKYVTSAPMPPEQAPGRYFAH 534
Qy 301 SRMLVNSIWEKGNLVTCTRVVHEALPG---SRTLEKS 334
Db 535 SILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKS 571

RESULT 7
Q8WUK1
ID Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-JUN-2002 (TremBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 21, Last annotation update)
DE Hypothetical 67.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR InterPro; IPR003599; IG_c1.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003596; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_5.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;
```

```
Query Match 26.3%; Score 488.5; DB 4; Length 613;
Best Local Similarity 31.2%; Pred. No. 4.3e-37;
Matches 105; Conservative 73; Mismatches 13; Indels 25; Gaps 10;
```

```
Qy 17 PVTII---PPTVKLFHSSCDPR---GDAHSTIQLCLVSGFSPAKVHVTVLWDQEAEN 69
Db 241 PLPVIAELPPKVSVF---VPPRDGFGNPKRS-KLICQATGFSPPQIQVSWLREGKQVGS 296
Qy 70 LFPYTT-----RPKREGGQTFSLQSEVNITQGWMSNTYTHVHNGSIP-EDSSRCS 123
Db 297 --GVTTDQVQAEAKESGPTTYKVTSLTIKESDWLSQSMFTCRVDHRLGTLTFOQNASSMCV 354
Qy 124 DDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVTVWRERKKSIGSASQST 183
Db 355 PQDQTAIRVFAIPSPFASIFLTSTLIKESDWLSQSMFTCRVDHRLGTLTFOQNASSMCV 414
Qy 184 KHHATTTSITSLPVDKADWIEGEGYQCRVDHPHPPKPIVRSITKLPGRKL-APEVYMLP 242
Db 415 SHPNATFSVAVGEASICEDDWNNGERFTCTVTHDLPSPKQTIISRPKGVALHRPDVYLLP 474
```

```
Qy 243 PSPETG---TTRTVCILRGFVPSISVQWLNNEDHTGHTTTRPKQKHGTDPSFFLY 300
Db 475 PAREQLNRESATITCLVTGFSFADVFVQWQMGQPLSPEKYVTSAPMPPEQAPGRYFAH 534
Qy 301 SRMLVNSIWEKGNLVTCTRVVHEALPG---SRTLEKS 334
Db 535 SILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKS 571

RESULT 8
Q96GA6
ID Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-CCELL;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
DR InterPro; IPR000005; HTHArac.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_5.
DR SMART; SM00408; IGc2; 2.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
```

```
Query Match 26.3%; Score 488.5; DB 4; Length 614;
Best Local Similarity 31.2%; Pred. No. 4.3e-37;
Matches 105; Conservative 73; Mismatches 134; Indels 25; Gaps 10;
```

```
Qy 17 PVTII---PPTVKLFHSSCDPR---GDAHSTIQLCLVSGFSPAKVHVTVLWDQEAEN 69
Db 241 PLPVIAELPPKVSVF---VPPRDGFGNPKRS-KLICQATGFSPPQIQVSWLREGKQVGS 297
Qy 70 LFPYTT-----RPKREGGQTFSLQSEVNITQGWMSNTYTHVHNGSIP-EDSSRCS 123
Db 298 --GVTTDQVQAEAKESGPTTYKVTSLTIKESDWLSQSMFTCRVDHRLGTLTFOQNASSMCV 355
Qy 124 DDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVTVWRERKKSIGSASQST 183
Db 356 PQDQTAIRVFAIPSPFASIFLTSTLIKESDWLSQSMFTCRVDHRLGTLTFOQNASSMCV 415
Qy 184 KHHATTTSITSLPVDKADWIEGEGYQCRVDHPHPPKPIVRSITKLPGRKL-APEVYMLP 242
Db 416 SHPNATFSVAVGEASICEDDWNNGERFTCTVTHDLPSPKQTIISRPKGVALHRPDVYLLP 475
Qy 243 PSPETG---TTRTVCILRGFVPSISVQWLNNEDHTGHTTTRPKQKHGTDPSFFLY 300
Db 476 PAREQLNRESATITCLVTGFSFADVFVQWQMGQPLSPEKYVTSAPMPPEQAPGRYFAH 535
Qy 301 SRMLVNSIWEKGNLVTCTRVVHEALPG---SRTLEKS 334
Db 536 SILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKS 572

RESULT 9
Q96AA6
ID Q96AA6 PRELIMINARY; PRT; 619 AA.
AC Q96AA6;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
```



```
Db 249 PNVVVF---VPPRDFSGPAPRKSKLICEATNFTPKPIITVSWLKDGLVESGFTTDPVTI 305
Qy 76 RPREGGQTFSLQSEVNITQGWMSNNTYCHVKNGSIF-EDSSRRCDDEPRVITVL 134
Db 306 ENKGSTPQTKVITLTITISEIDWLNVTCDVHRGLTFLKNVSTCAASPSTDLITFT 365
Qy 135 IPPSPDLIYENCTPKLTCLVLDSSEENITVWVRKKSIGSASQSRSTKHHHTTSITS 194
Db 366 IPPSPADIFLSKANLTCVLVSNLTIYETLNISWASQSGEPLTKIKIMESHPNGFTSAK 425
Qy 195 ILPVDKADWIEGQCRVDHDPFKPIVRSITKLPKG--RLAPEVYMLPPSPETG--T 250
Db 426 VASVCVEDWNRKEFVCTVTHRDLSPQKFKISK-PNEVHKHPPAVALLPPAREQLNRE 484
Qy 251 TRVTCLIRGFYPSISVQWLNNEDHTGHHTTRPKQDHGTDPSFFLYSRLVNKSIW 310
Db 485 SATVTCLVKGFSADISVQWLQGLLPQEKYVTSAPMPGAPGFYFTHSILITVTEBW 544
Qy 311 EKNLVTCTVWHEALP---GSRTLEKS 334
Db 545 NSGETYTCVWGHEALPHLVTRTVDKS 571

RESULT 12
Q8TC63 PRELIMINARY; PRT; 473 AA.
ID Q8TC63
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical 52.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 24.5%; Score 455; DB 4; Length 473;
Best Local Similarity 33.4%; Pred. No. 4.2e-34;
Matches 115; Conservative 67; Mismatches 128; Indels 34; Gaps 12;

Qy 18 VTIIPTVK---LFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW---LVDGQEAENL 70
Db 142 VSVSPASTKGPSVFLPAPCSRSTSESTAALGLVKDYFPEPTVTVSWNSGALTSG---VHT 198
Qy 71 PPTTRPKREGQTFSLQSEVNITQGWMSNNTYCHVKNGSIFEDSSRRCDDEP--- 127
Db 199 FPAVL---QSSGLSLSSVTVFPSS-LGTQTYICNVNKHPSNTKVDKVEPKSCDKTH 253
Qy 128 -----RGVITYLIPSPDL-LYENGTPKLTCLVLDSSE-NITVWVRKKSIGS 177
Db 254 SCPAPEFLGGPSVFLPPPKDITMISRTPEVTCVVVDVSDPEQVFNWYVDGVEVHNA 313
Qy 178 ASQRTSKHHHTSITSILPVDAKWIEGQCRVDHDPFKPIVRSITKLPKRLAPE 237
Db 314 KTKPREEQNSTYRVVSVLTVLHQDLNKGKCKVSNKALDPAIEKTLISKAKGQPR 373
Qy 238 VYMLPPSPPEE-TGTRTTRVTCIRGFYPSISVQWLNNEDHTGHHTTRPKQDHGTDPS 296
Db 374 VYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN--NYKTTTPVPLD--SDGS 429
Qy 297 PFLYSRLVNKSIWEKGNLVTCTVWHEALPGSRTLEKSLHYSAG 340
Db 430 FFCYSLRLTVDKSRWQGNVFCVSNVHEALHNHYT--OKSLSLSIG 472
```

```
RESULT 13
Q8TC77 PRELIMINARY; PRT; 471 AA.
ID Q8TC77
AC Q8TC77;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAH24289.1; -.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 23.8%; Score 441.5; DB 4; Length 471;
Best Local Similarity 31.7%; Pred. No. 7.6e-33;
Matches 110; Conservative 73; Mismatches 127; Indels 37; Gaps 13;

Qy 18 VTIIPTVK---LFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW---LVDGQEAENL 70
Db 137 VTVSASTKGPSVFLPAPCSRSTSGTAAALGLVKDYFPEPTVTVSWNSGALTSG---VHT 193
Qy 71 PPTTRPKREGQTFSLQSEVNITQGWMSNNTYCHVKNGSIFE-----DSSR 120
Db 194 FPAVL---QSSGLSLSSVTVFPSS-LGTQTYICNVNKHPSNTKVDKVEPKSCDKTH 248
Qy 121 RC-----SDSEPRGVITYLIPSPDL-LYENGTPKLTCLVLDSSE-NITVWVRKKKS 174
Db 249 TCPPCAPELGGPSVFLPPPKDITMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEV 308
Qy 175 IGSASQRTSKHHHTSITSILPVDAKWIEGQCRVDHDPFKPIVRSITKLPKRL 234
Db 309 HNAKTKPREEQNSTYRVVSVLTVLHQDLNKGKCKVSNKALDPAIEKTLISKAKGQPR 368
Qy 235 APEVYMLPPSPPEE-TGTRTTRVTCIRGFYPSISVQWLNNEDHTGHHTTRPKQDHGT 293
Db 369 EPQVITYLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN--NYKTTTPVPLD--S 424
Qy 294 DPFSPFLYSRLVNKSIWEKGNLVTCTVWHEALPGSRTLEKSLHYSAG 340
Db 425 DGSFFLYSLKLTVDKSRWQGNVFCVSNVHEALHNHYT--OKSLSLSPG 470

RESULT 14
Q9RIA4 PRELIMINARY; PRT; 437 AA.
ID Q9RIA4
AC Q9RIA4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Gammal heavy chain of Mab7 (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7) its light and heavy chains) and construction of a single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
```

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DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; Ig_Like; 2.
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3BE7D697C CRC64;

Query Match      23.4%; Score 435; DB 11; Length 437;
Best Local Similarity 31.2%; Pred. No. 2.8e-32;
Matches 109; Conservative 66; Mismatches 134; Indels 40; Gaps 13;

Qy 16 GPVTII-----PPTVKLFHSSCDPRGDAHSTTQLLCLVSGFSPAKVHVTW-----LVD 63
Db 104 GPGTLVTVSAAKTTPSV--YPLAPGSAQAQNSMTLGLVKVGYPPEPTVTWNSGSLSS 161

Qy 64 QEAENLFPYTRPKREGGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIF----- 115
Db 162 G---VHTFPVAVLQ-----SDLYTLSSSVTPSSTW-PSETVTCNVAHPASSTKVDKIVP 212

Qy 116 -EDSSRRCSDDPRGVITYLPPSPLD-LYENGTPKLTCLVLDLESE-NITVTWVRERK 172
Db 213 RDGCKPCICTVPEVSSVFIPFPKPKDVLITLTPKVTCCVVVDISKDDPEVQFSWFVDDV 272

Qy 173 KSIGASQRSTKHHATTITSILPVDADKDWIEGEGYQCRVDHPHPKPIVRSITKLPGRK 232
Db 273 EVHTAQTPREQFNSTFRSVSELPIMHQDWLNGKEFKRCVNSAAPPAPIEKTISTKTGR 332

Qy 233 RLAEVYMLPPSPETGTTR-TVTCLIRGFYPSEISVQWLPNNEEDHTGHHTTTRPKQKH 291
Db 333 PKAPQVYTIPTPPKEQMAKDKVSLTCMTDFFPEDITVEQWNGQP--AENYKNTQPIMD- 389

Qy 292 GTDPSFFLYSRMLNKSWEKGNLVTCTVWVHEALPGSRTLEKSLHYSAG 340
Db 390 -TDGSFYFYKLNQVQSNWEAGNTFTCSVLHEGLHNHHT-EKSLSHSPG 436

RESULT 15
Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to RIKEN cDNA 1810060009 gene.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AA03435.1; -.
DR HSSP; P01842; 7FAB
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; Ig_Like; 1.
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
```

```
Query Match      23.4%; Score 434.5; DB 11; Length 463;
Best Local Similarity 31.6%; Pred. No. 3.4e-32;
Matches 110; Conservative 65; Mismatches 136; Indels 37; Gaps 13;

Qy 9 TSLSPESGPVTIIPPTVKLFHSSCDPRGDAHSTTQLLCLVSGFSPAKVHVTW-----LYDG 64
Db 136 TVSAAKTTPPSVYP----LAPGSA---AQTNSMTLGLVKVGYPPEPTVTWNSGSLSSG 188

Qy 65 QEAENLFPYTRPKREGGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIF----- 115
Db 189 ---VHTFPVAVLQ-----SDLYTLSSSVTPSSTW-PSETVTCNVAHPASSTKVDKIVP 239

Qy 116 EDSSRRCSDDPRGVITYLPPSPLD-LYENGTPKLTCLVLDLESE-NITVTWVRERK 173
Db 240 DCGCKPCICTVPEVSSVFIPFPKPKDVLITLTPKVTCCVVVDISKDDPEVQFSWFVDDVE 299

Qy 174 SIGASQRSTKHHATTITSILPVDADKDWIEGEGYQCRVDHPHPKPIVRSITKLPGRK 233
Db 300 VHTAQTPREQFNSTFRSVSELPIMHQDWLNGKEFKRCVNSAAPPAPIEKTISTKTGRP 359

Qy 234 RLAEVYMLPPSPETGTTR-TVTCLIRGFYPSEISVQWLPNNEEDHTGHHTTTRPKQKH 292
Db 360 KAPQVYTIPTPPKEQMAKDKVSLTCMTDFFPEDITVEQWNGQP--AENYKNTQPIMD-- 415

Qy 293 TDPSEFFLYSRMLNKSWEKGNLVTCTVWVHEALPGSRTLEKSLHYSAG 340
Db 416 TDGSFYFYKLNQVQSNWEAGNTFTCSVLHEGLHNHHT-EKSLSHSPG 462
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Search completed: March 8, 2003, 07:49:25
Job time : 35 sec

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OM protein - protein search, using sw model

Run on: March 8, 2003, 07:43:50 ; Search time 13 Seconds
(without alignments)
1087.956 Million cell updates/sec

Title: us-09-401-636-4

Perfect score: 1858

Sequence: 1 EFHHHHHTLSLPESGPVTI.....HEALPGSRTLEKSLHYSAGN 341

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1051	56.6	429	1 EPC_RAT	P01855 rattus norv
2	940.5	50.6	421	1 EPC_MOUSE	P06336 mus musculus
3	745	40.1	428	1 EPC_HUMAN	P01854 homo sapien
4	499	26.9	454	1 MUC_HUMAN	P01871 homo sapien
5	490	26.4	479	1 MUCM_RABIT	P04221 oryctolagus
6	488	26.3	458	1 MUC_RABIT	P03988 oryctolagus
7	484.5	26.1	391	1 MUCB_HUMAN	P04220 homo sapien
8	468	25.2	326	1 GC2_HUMAN	P01859 homo sapien
9	464.5	25.0	450	1 MUC_CANFA	P01874 canis fami
10	455.5	24.5	455	1 MUC_MOUSE	P01872 mus musculus
11	455.5	24.5	476	1 MUCM_MOUSE	P01873 mus musculus
12	451.5	24.3	327	1 GC4_HUMAN	P01861 homo sapien
13	449.5	24.2	457	1 MUC_SUNMU	P02768 suncus muri
14	440.5	23.7	330	1 GC1_HUMAN	P01857 homo sapien
15	433.5	23.3	454	1 MUC_MESAU	P06337 mesocricetu
16	426	22.9	322	1 GCA_RAT	P02760 rattus norv
17	424.5	22.8	329	1 GGC_RAT	P02762 rattus norv
18	424.5	22.8	335	1 GCAB_MOUSE	P01864 mus musculus
19	423	22.8	326	1 GC1_RAT	P02759 rattus norv
20	422	22.7	323	1 GC_RABIT	P01870 oryctolagus
21	419	22.6	329	1 GC2_CAVPO	P01862 cavia porce
22	410	22.1	324	1 GC1_MOUSE	P01868 mus musculus
23	410	22.1	393	1 GC1M_MOUSE	P01869 mus musculus
24	408.5	22.0	329	1 GC3_MOUSE	P22436 mus musculus
25	405	21.8	336	1 GCB_MOUSE	P01866 mus musculus
26	405	21.8	405	1 GCBM_MOUSE	P01867 mus musculus
27	403.5	21.7	398	1 GC3M_MOUSE	P03987 mus musculus
28	394	21.2	330	1 GC4A_MOUSE	P01863 mus musculus
29	394	21.2	399	1 GCAM_MOUSE	P01865 mus musculus
30	386	20.8	290	1 GC3_HUMAN	P01860 homo sapien
31	386	20.8	438	1 HVC2_HETFR	P23085 heterodontu
32	381.5	20.5	333	1 GCB_RAT	P02761 rattus norv
33	373	20.1	438	1 HVC5_HETFR	P23087 heterodontu

RESULT 1

EPC_RAT	ID	EPC_RAT	STANDARD;	PRT;	429 AA.
AC	P01855;	AC			
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	ig epsilon chain C region.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).				
RC	STRAIN=LOU/C/WSL;				
RX	MEDLINE=83064537; PubMed=6292865;				
RA	Hellman L., Petterson U., Engstroem A., Karlsson T., Bennich H.;				
RT	"Structure and evolution of the heavy chain from rat immunoglobulin E";				
RT	E.,"				
RL	Nucleic Acids Res. 10:6041-6049(1982).				
RN	[2]				
RP	SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).				
RX	MEDLINE=83182019; PubMed=6820340;				
RA	Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;				
RT	"A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, identification, and DNA sequence.";				
RL	DNA 1:335-343(1982).				
RN	[3]				
RP	SEQUENCE OF 205-306 FROM N.A.				
RX	MEDLINE=82174576; PubMed=6803238;				
RA	Hellman L., Petterson U., Bennich H.;				
RT	"Characterization and molecular cloning of the mRNA for the heavy (epsilon) chain of rat immunoglobulin E.,"				
RL	Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).				
CC	-----				
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CC	-----				
CC	EMBL; J00744; AAA41379.1; ALT_INIT.				
DR	PIR; A02143; EHRT.				
DR	HSSP; P01854; 1IGE.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003597; Ig_ci.				
DR	InterPro; IPR003600; Ig_like.				
DR	PFam; PF00047; Ig; 4.				
DR	SMART; SM00410; IG-like; 3.				
DR	SMART; SM00407; IGG1; 1.				
DR	PROSITE; PS00290; IG_MHC; 3.				
KW	Immunoglobulin domain; Immunoglobulin C region.				
FT	NON TER 1				
FT	CONFLICT 168 168 R -> N (IN REF. 2).				

ALIGNMENTS

34	373	20.1	461	1	HVCM_HETFR	P23088 heterodontu
35	363	19.5	393	1	HVC3_HETFR	P23086 heterodontu
36	355	19.1	340	1	ALC2_HUMAN	P01877 homo sapien
37	348	18.7	370	1	HVC1_HETFR	P23084 heterodontu
38	346.5	18.6	353	1	ALC1_HUMAN	P01876 homo sapien
39	336.5	18.1	353	1	ALC1_GORGO	P20758 gorilla gor
40	334.5	18.0	446	1	MUC_CHICK	P01875 gallus gall
41	323	17.4	344	1	ALC_MOUSE	P01878 mus musculus
42	270.5	14.6	481	1	MUCM ICTPU	P23735 ictalurus p
43	237.5	12.8	299	1	ALC_RABIT	P01879 oryctolagus
44	210	11.3	383	1	DTC_HUMAN	P01880 homo sapien
45	160	8.6	103	1	LAC_CHICK	P20763 gallus gall

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FT CONFLICT 308 308 P -> L (IN REF. 2).
SQ SEQUENCE 429 AA; 48671 MW; D2970B34EF8A72B0 CRC64;

Query Match 56.6%; Score 1051; DB 1; Length 429;
Best Local Similarity 62.6%; Pred. No. 3.3e-72;
Matches 206; Conservative 35; Mismatches 78; Indels 10; Gaps 3;

Qy 17 PVTIIPPTVKLFHSSCDPRGDAHSITQLCLVSGSPAKVHVHTVLVDGQEAENLFPYTTR 76
Db 97 PYNITKPTVDLLHSSCDPNA-FHSTIQLYCFVYGHQNDVSIHLMDDRKI-----YETH 150
Qy 77 PK-----REGGQFSLQSEVNIQOGWMSNTYTCHVKGNSIFEDSSRCSDDPRGVIT 132
Db 151 AQNVLIKEGKLASYSLRNITQQQWMSSEFTCKVTSQGENYWAHTRCSDDEPRGVIT 210
Qy 133 YLIPSPDLVYENGTPKLTCLVLDLESENIITVWVRERKKSIGSASQSTKHHATTSI 192
Db 211 YLIPSPDLVYENGTPKLTCLVLDLESENIITVWVRERKKSIGSASQSTKHHATTSI 270
Qy 193 TSILPVDAKDWIEGEGYQCRVDHPHPKPIVRSITKLPKRLAPEVYMLPPSPETGTTR 252
Db 271 TSILPVDAKDWIEGEGYQCRVDHPHPKPIVRSITKLPKRLAPEVYMLPPSPETGTTR 330
Qy 253 TVTCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKOHGTDPSPFLYSRLVNSKIWEK 312
Db 331 TLTCLIQNFPPEDISVQWLDKSLPKSOHSITTPKYNQSNQRPFIISRLVTKALWTQ 390
Qy 313 GNLVTCRVVHEALPGSRITLKSLSHYSAGN 341
Db 391 TKQFTCRVTHEALREPKLERTISLGN 419

RESULT 2
EPC_MOUSE
ID EPC_MOUSE STANDARD; PRT; 421 AA.
AC P06336; P01856;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig epsilon chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84236092; PubMed=6329728;
RA Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
RT "The nucleotide sequence of the mouse immunoglobulin epsilon gene:
RT comparison with the human epsilon gene sequence.";
RL EMBO J. 1:1117-1123(1982).
RN [2]
RP REVISIONS.
RA Honjo T.;
RL Submitted (APR-1986) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 34-421 FROM N.A.
RX MEDLINE=83117774; PubMed=6818553;
RA Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
RT "Cloning and nucleotide sequence of mouse immunoglobulin epsilon
RT chain cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01857; CAA25977.1; -.
DR EMBL; X01857; X01857; Muridae; Murinae; Mus.
DR EMBL; X01857; X01857; Muridae; Murinae; Mus.
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DR PIR; A02145; EHMSS.
DR PIR; A02144; EHMSS.
DR HSP; P01854; ILGE.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00410; Ig_Like; 2.
DR SMART; SM00407; IGL1; 2.
DR PROSITE; PS00290; Ig_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 90 CH1.
FT DOMAIN 91 197 CH2.
FT DOMAIN 198 304 CH3.
FT DOMAIN 305 421 CH4.
FT DISULFID 23 75 BY SIMILARITY.
FT DISULFID 121 180 BY SIMILARITY.
FT DISULFID 226 285 BY SIMILARITY.
FT DISULFID 330 392 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 421 AA; 47320 MW; 8F909E1F3A06B47 CRC64;

Query Match 50.6%; Score 940.5; DB 1; Length 421;
Best Local Similarity 55.2%; Pred. No. 6.9e-64;
Matches 191; Conservative 46; Mismatches 100; Indels 9; Gaps 5;

Qy 2 FHHHHHTLSLPES-----GPVTIIPPTVKLFHSSCDPRGDAHSITQLCLVSGSPAKV 56
Db 73 FTCHVTHPPSFNESTRILVRPNVITEPTLELLHSSCDPNA-FHSTIQLYCFIYGHILNDV 131
Qy 57 HVTWLVDGQEAENLFPYTTRPKRGQTFSLQSEVNIQOGWMSNTYTCHVKGNSIFE 116
Db 132 SVSWMDDRETITDIAQTVLKEE-GKLASTCSKLNITEQQWMSSEFTCKVTSQVDYL 190
Qy 117 DSSRCSDDPRGVITLYLIPSPDLVYENGTPKLTCLVLDLESENIITVWVRERKKSIG 176
Db 191 AHTRRCPDHEPRGVITLYLIPSPDLVYENGTPKLTCLVLDLESENIITVWVRERKKSIG 249
Qy 177 SASQSTKHH-HATTSTISILPVDAKDWIEGEGYQCRVDHPHPKPIVRSITKLPKELA 235
Db 250 SASQWYTKHNNATTSITSLPVVAKDWIEGEGYQCIVDHPDPKPIVRSITKTPGQSA 309
Qy 236 PEVYMLPPSPETGTTRTCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKOHGTDP 295
Db 310 PEVYVFPPEESEDKRTLTCLIQNFPPEDISVQWLDGKLSNSQHSSTTTPKLSNGSNQ 369
Qy 296 SFFLYSRMLVNSKIWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 341
Db 370 GFFIFSRLEVAKTLWTKQKQFTQCVIHEALQKPRKLEKTISTSLGN 415

RESULT 3
EPC_HUMAN
ID EPC_HUMAN STANDARD; PRT; 428 AA.
AC P01854;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig epsilon chain C region.
GN IGHE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN [3].
RP REVISIONS (GAL).
RX MEDLINE=81066716; PubMed=6777162;
RA Mihaesco E., Barnikol-Watanabe S., Barnikol H.U., Mihaesco C.,
RN Hiltschmann N.;
RT "The primary structure of the constant part of mu-chain-disease
protein BOT";
RL Eur. J. Biochem. 111:275-286(1980).
RN [4].
RP SEQUENCE (WALDENSTROM'S OU), DISULFIDE BONDS, AND CARBOHYDRATES.
RX MEDLINE=74005511; PubMed=4742735;
RA Putnam F.W., Florent G., Paul C., Shinoda T., Shimizu A.;
RT "Complete amino acid sequence of the mu heavy chain of a human IgM
immunoglobulin";
RL Science 182:287-291(1973).
RN [5].
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=82059479; PubMed=6795593;
RA Rabbitts T.H., Forster A., Milstein C.P.;
RT "Human immunoglobulin heavy chain genes: evolutionary comparisons of
C mu, C delta and C gamma genes and associated switch sequences.";
RL Nucleic Acids Res. 9:4509-4524(1981).
RN [6].
RP SEQUENCE OF 299-387 AND 438-454 FROM N.A.
RX MEDLINE=81077306; PubMed=677778;
RA Dolby T.W., Devuono J., Croce C.M.;
RT "Cloning and partial nucleotide sequence of human immunoglobulin mu
chain cDNA from B cells and mouse-human hybridomas";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6027-6031(1980).
CC -!- MISCELLANEOUS: ALL 4 COMBINATIONS OF THE S/G & V/G POLYMORPHISMS
CC AT POSITIONS 192 AND 216 HAVE BEEN OBSERVED IN HUMAN MU CHAINS.
CC -----
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CC -----
DR EMBL; X17115; CAA34971.1; ALT SEQ.
DR EMBL; X57086; -: NOT_ANNOTATED_CDs.
DR PIR; A02162; MHU.
DR HSSP; P01857; 1FC1.
DR Genew; HGNC:5541; IGMM.
DR MIM; 147020; -.
DR GlycoSuiteDB; P01871; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGCI; 3.
DR PROSITE; PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 105
FT DOMAIN 106 218
FT DOMAIN 219 324
FT DOMAIN 325 454
FT DISULFID 14 14
FT DISULFID 28 98
FT DISULFID 135 198
FT DISULFID 215 215
FT DISULFID 245 304
FT DISULFID 292 292
FT 352 414
FT DISULFID 453 453
FT CARBOHYD 46 46
FT CARBOHYD 210 210

FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .).
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .).
FT VARIANT 192 192 /FTID=CAR_000219.
FT S->G.
FT VARIANT 216 216 /FTID=VAR_003903.
FT V->G.
SQ SEQUENCE 454 AA; 49556 MW; 21EC72EADC56922E CRC64;
Query Match 26.9%; Score 499; DB 1; Length 454;
Best Local Similarity 31.5%; Pred. No. 1.5e-30;
Matches 106; Conservative 72; Mismatches 135; Indels 24; Gaps 9;
Qy 17 PVTII---PPTVKLFHSCDPR----GDAHSTIQLCLVSGFSPAKVHVTVLWVDCQAEEN 69
Db 102 PLPVIAELPPKVSF---VPPRDGFFGNPRSKSLICATQATGSPRQIQVSLREGQVGS 158
Qy 70 LFPYTT----RPKREGGQTFSLQSEVNIQTQWMSNTYCHVKHGSIF-EDSSRCS 123
Db 159 --GVTTDOVQAEAKESGPTTKYKSTLTIKESDWLSQSMFTRVDHRLTQQNASSMVCV 216
Qy 124 DDEPRGVITYLIPESPLDLYENGTPKLTCLVLDLSEENITVTWVRKKSIGSASQST 183
Db 217 PQDTAIRVFAIPPSFASIFLTSTKLTCLVTLTVDTSVTSITRONGEAVKTHNISE 276
Qy 184 KHHATTSITSILPVDAKDWIEGEGYQCRVDHPHPPRIVRSITKLPKRL-APEVYMLP 242
Db 277 SHPNATFSVAGEASICEDDMNSGERFCTVTHTDLPSPKQTSIRPKGVALLHRPDVYLLP 336
Qy 243 PSPETG--TTRTVTCLIRGFPSEISVOWLPNNEEDHTGHTTTRPKQDHDGTPSPFELY 300
Db 337 PARQLNRESATITCLVTGSPADVFQVMQORGLSPKQVTSAPNPEQAPGRYFAH 396
Qy 301 SRMLVNKSIMWKNLVTCTRVVHEALPG---SRTLEKS 334
Db 397 SILTVSEEMWTGTYTCVVAHEALPNRVTERTVDKS 433
RESULT 5
MUCM RABIT STANDARD; PRT; 479 AA.
AC P0422L;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig mu chain C region membrane-bound form.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A. (A2 ALLOTYPED).
RX MEDLINE=84088930; PubMed=6418803;
RA Bernstein K.B., Alexander C.B., Reddy E.P., Mage R.G.;
RT "Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain
of VHA2 allotype: comparisons with VHA1 and membrane mu sequences.";
RL J. Immunol. 132:490-495(1984).
CC -!- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LYMPHOCYTES
CC SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SECRETION OF IGM.
CC THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER IN THEIR C-
CC TERMINAL SEGMENTS.
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CC -----
DR EMBL; K01357; AAA31293.1; -.
DR PIR; A02165; MHRBM.

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DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00410; IG like; 2.
DR SMART; SM00407; IGL; 2.
DR PROSITE; PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON TER 1
FT DOMAIN 1 106 CH1.
FT DOMAIN 107 222 CH2.
FT DOMAIN 223 327 CH3.
FT DOMAIN 328 458 CH4.
FT TRANSMEM 459 476 POTENTIAL.
FT DISULFID 14 14 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
FT DISULFID 28 90 BY SIMILARITY.
FT DISULFID 137 200 BY SIMILARITY.
FT DISULFID 219 219 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 249 308 BY SIMILARITY.
FT DISULFID 356 418 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 296 296 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 479 AA; 52351 MW; 689C637A7B19FC CRC64;

Query Match 26.4%; Score 490; DB 1; Length 479;
Best Local Similarity 32.4%; Pred. No. 7.7e-30;
Matches 114; Conservative 62; Mismatches 150; Indels 18; Gaps 8;

Qy 5 HHHHTLSLPESGPV-TIIPPTVKLFHSSCDP-RGDAHSTIQLCLVSGFSPAKVHTWLV 62
Db 94 HSNRNDRLVSPFVDSLPNNVSPFIPPRDSFGSGTRKSLRICQATGSPKQISVWLR 153

Qy 63 DQQAEN---LFPYTRPRKREGQTFSLQSEVNITQGWMSNTYTCVKGNGSIFEDS- 118
Db 154 DQKVESGLVKPVEAETKGAGPATFSISSMLTITSDLSQSLYTCRVDHGRGIFDKV 213

Qy 119 ---SRCSDDPRGVITYLIPSPDLVNGTPKLCLVLDLESENITVWVRKKSIG 176
Db 214 SMSSECSSTPSPGIQVFFIAPSFADTFLSKSARLCLVTLDTLTYGSLNISWASHNGKALD 273

Qy 177 SASQBSTKHHTATTSITSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPKRLA- 235
Db 274 THMNITESHPNATFSAMGEASVCAEDWESGQFTCTVTHADLPFLKHTISK--SREVAK 331

Qy 236 --PEVYMLPPSPPEE--TGTTRTVTCLIRGFYSPSEISVQWLPNNEEDTGHHTTTRPQKH 291
Db 332 HPPAVYVLPAREQLVRESATVCLVGFSPADVFVQVQQRQGLSSDKYTSAPAPEP 391

Qy 292 GTPDSFFLYSRMLNKSWEKGNLTCRVVHEALP---GSRITLEKSLHYSAG 340
Db 392 QAPGLYPTHSTLTVEEDWNSGETTCVVGHEALPHMVTERTVDSKTEGEVG 443

RESULT 6
MUC_RABIT
AC P03988; STANDARD; PRT; 458 AA.
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig mu chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_taxid=9986;
RN [1]

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RP SEQUENCE FROM N.A. (A2 ALLOTYPED).
RX MEDLINE=84089930; PubMed=6418803;
RA Bernstein K.B., Alexander C.B., Reddy E.P., Mage R.G.;
RT "Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain
of VHa2 allotype: comparisons with VHa1 and membrane mu sequences.";
RL J. Immunol. 132:490-495(1984).
CC -!- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LYMPHOCYTES
CC SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SECRETION OF IGM.
CC THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER IN THEIR C-
CC TERMINAL SEGMENTS.
CC -----
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CC -----
CC EMBL; K01357; -; NOT_ANNOTATED_CDS.
CC PIR; A02164; MHRB.
CC HSSP; P01842; 7FAB.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003597; Ig_c1.
CC InterPro; IPR003600; Ig_like.
CC Pfam; PF00047; Ig; 4.
CC SMART; SM00410; IG like; 2.
CC SMART; SM00407; IGL; 2.
CC PROSITE; PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing.
FT NON TER 1
FT DOMAIN 1 106 CH1.
FT DOMAIN 107 222 CH2.
FT DOMAIN 223 327 CH3.
FT DOMAIN 328 458 CH4.
FT DISULFID 14 14 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
FT DISULFID 28 90 BY SIMILARITY.
FT DISULFID 137 200 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 219 219 BY SIMILARITY.
FT DISULFID 249 308 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 296 296 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 356 418 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 458 AA; 49897 MW; F338D6A3B28E4864 CRC64;

Query Match 26.3%; Score 488; DB 1; Length 458;
Best Local Similarity 32.7%; Pred. No. 1e-29;
Matches 114; Conservative 62; Mismatches 149; Indels 24; Gaps 9;

Qy 5 HHHHTLSLPESGPV-TIIPPTVKLFHSSCDP---GDAHSTIQLCLVSGFSPAKVHT 59
Db 94 HSNRNDRLVSPFVDSLPNNVSPF---IPRDSFGSGTRKSLRICQATGSPKQISV 150

Qy 60 WLVDQQAEN---LFPYTRPRKREGQTFSLQSEVNITQGWMSNTYTCVKGNGSIFE 116
Db 151 WLRDQKVESGLVKPVEAETKGAGPATFSISSMLTITSDLSQSLYTCRVDHGRGIFD 210

Qy 117 DS---SRCSDDPRGVITYLIPSPDLVNGTPKLCLVLDLESENITVWVRK 173
Db 211 KVSMSSECSSTPSPGIQVFFIAPSFADTFLSKSARLCLVTLDTLTYGSLNISWASHNGK 270

Qy 174 SIGSQBSTKHHTATTSITSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGR 233
Db 271 ALDTHMNITESHPNATFSAMGEASVCAEDWESGQFTCTVTHADLPFLKHTISK--SRE 328

Qy 234 LA---PEVYMLPPSPPEE--TGTTRTVTCLIRGFYSPSEISVQWLPNNEEDTGHHTTTRPQ 288

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RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
RN [10]
RP DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).
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CC -----
DR EMBL; J00230; AAB59393.1; -.
DR PIR; A02148; G2HU.
DR HSP; P01857; 1FC1.
DR Genew; HGNC:5526; IGHG2.
DR MIM; 147110; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGL1; 2.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON TER 1 1
FT DOMAIN 1 98
FT CH1.
FT DOMAIN 99 110
FT HINGE.
FT DOMAIN 111 219
FT CH2.
FT DOMAIN 220 326
FT CH3.
FT DISULFID 14 14
FT INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 102 102
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 103 103
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT SITE 156 156
FT SITE 326 326
FT MOD RES 326 326
FT VARIANT 60 60
FT CONFLICT 109 109
FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
Query Match 25.2%; Score 468; DB 1; Length 326;
Best Local Similarity 34.4%; Pred. No. 2.28-28;
Matches 111; Conservative 66; Mismatches 116; Indels 30; Gaps 12;
Qy 35 RGDHSTTQLLCVSGFSPAKVHTW----LVDGQAEHLFPYTRPRKREGQTSLOSE 90
Db 16 RSTSESTAALGCLVKDYFPEPTVSWNSGALTSG---VHTPAVL-----QSSGLYSLSV 68
Qy 91 VNITQGMNSNTYCHVKH---NGSIFEDSSRRCSDDP-----RGVITYLIPPSPL 140
Db 69 VTPSSNF-GTQTYTCNVDHKPSNTKVDKTVKCCVCPAPPVAGPSVFLFPKPK 127
Qy 141 D-LYENGTPKLTCLVLDSESE-NITVTWVRERKKSIGASORSTKHHHTTSILPV 198
Db 128 DTLMSIRTPVETCVVDVSHEDPEVQFNMYDGVVHNKAKTPREEQFNSTFRVVSILT 187
Qy 199 DAKWIEGEGQCRVDHPFKPIVRSITKLPGKRLAPEVYMLPSPBE-TGTTTIVTCL 257
Db 188 VHQDWLNKEVKCKVSNKGLPAPIEKTISKYQGPREFQVYTLPPSREMTKNQVSLCL 247
Qy 258 IRGFYPSISVQWLPNNBEDHTGHTTTPQKDHGTDPSFFLYSRMLNYSIWEKGNLVT 317

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Db 248 VKGYPSDIAVWESSNGQPEN--NYKTPPMLD--SDGSFFLYSKLTVDKRWQGNVFS 303
Qy 318 CRVVHEALPGSRTLEKSLHYSAG 340
Db 304 CSVMHEALHNHYT-QKSLSLSPG 325
RESULT 9
MUC_CANFA
ID MUC_CANFA STANDARD; PRT; 450 AA.
AC P01874;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig mu chain C region.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE OF 1-177 (MOO).
RX MEDLINE=80077682; PubMed=117299;
RA McCumber L.J., Capra J.D.;
RT "The complete amino-acid sequence of a canine mu chain.";
RL Mol. Immunol. 16:565-570(1979).
RN [2]
RP SEQUENCE OF 178-450 (MOO).
RX MEDLINE=78180587; PubMed=653360;
RA Wasserman R.L., Capra J.D.;
RT "Amino acid sequence of the Fc region of a canine immunoglobulin M:
RT interspecies homology for the IgM class.";
RL Science 200:1159-1161(1978).
DR PIR; A02169; MHDG.
DR HSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00410; IG_Like; 2.
DR SMART; SM00407; IGL1; 2.
DR PROSITE; PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON TER 1 1
SQ SEQUENCE 450 AA; 48895 MW; 9D460DA9D1012F5D CRC64;
Query Match 25.0%; Score 464.5; DB 1; Length 450;
Best Local Similarity 31.8%; Pred. No. 6e-28;
Matches 109; Conservative 69; Mismatches 136; Indels 29; Gaps 12;
Qy 10 LSLPE--SGPVITIPPTVKLFHSSCDPRGDAHSTTQLLCVSGFSPAKVHTW-LVDGQE 66
Db 106 LTLPEVSG---FIPPRDAFFG---BPRKS-----QLICQASGFSRQV---WSLRDGKQ 151
Qy 67 AENLFPYTT-----RPRKGGQTSLOSEVNITQGMNSNTYCHVKHNSIP-EDSSR 120
Db 152 IES--GVTTNEVZAKZSGPTTKVTSMLTQEDAWLSQSFTCKVSHRGLTFQONASS 209
Qy 121 RCDDEPRGVITYLIPPSPLDYENGTPKLTCLVLDSESENIITVWVRERKKSIGSASQ 180
Db 210 MCTSDQPGVIGISFTIPPSFASIFNTKSAKSLCLVTLATYDSVTISWTREENGALKHTN 269
Qy 181 RSTGHHHTTITSILPYDAKDWTEGEGYQCRVDHPFKPIVRSITKLPGKRL-APEVY 239
Db 270 ISEHPNGTTFAMGEATVCVWEESGEQFTCTVHTDLPVLKQTIISRPKGVAVHMPVY 329
Qy 240 MLPPSPETG--TTRTVCILIRGFYPSISVQWLPNNBEDHTGHTTTPQKDHGTDPSF 297
Db 330 VLPPSREQLDRESATLSCLVTGYSPDPVFVQVQWQKGPVPPDSVYTSAPMPQPAPGLY 389
Qy 298 FLYSRMLNYSIWEKGNLVTCTRVHREALPGSRTLEKSLHYSAG 340
Db 390 FAHSILTYSSEBNAGETVTCVAHESLP-NRVTERSVDKSTG 431

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RESULT 10
MUC MOUSE
ID - MUC MOUSE STANDARD; PRT; 455 AA.
AC P01872;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig mu chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076590; PubMed=6255422;
RA Kawakami T., Takahashi N., Honjo T.;
RT "Complete nucleotide sequence of mouse immunoglobulin mu gene and
RT comparison with other immunoglobulin heavy chain genes.";
RL Nucleic Acids Res. 8:3933-3945 (1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82051295; PubMed=6795090;
RA Goldberg G.I., Vanin E.F., Zrolka A.M., Blattner F.R.;
RT "Sequence of the gene for the constant region of the mu chain of
RT Balb/c mouse immunoglobulin.";
RL Gene 15:33-42 (1981).
RN [3]
RP SEQUENCE FROM N.A. (MYELOMA TPC183).
RX MEDLINE=81165562; PubMed=6260591;
RA Auffray C., Rougeon F.;
RT "Nucleotide sequence of a cloned cDNA corresponding to secreted mu
RT chain of mouse immunoglobulin.";
RL Gene 12:77-86 (1980).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).
RX MEDLINE=79223904; PubMed=111247;
RA Kehry M.R., Sibley C.H., Fuhrman J.S., Schilling J.W., Hood L.E.;
RT "Amino acid sequence of a mouse immunoglobulin mu chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:2932-2936 (1979).
RN [5]
RP REVISION (MOPC 104E).
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424 (1982).
CC -!- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LYMPHOCYTES
CC SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SECRETION OF IGM.
CC THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER IN THEIR C-
CC TERMINAL SEGMENTS.
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CC -----
CC EMBL; V00827; -, NOT_ANNOTATED_CDS.
DR PIR; A02166; MHMS.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00410; Ig_Like; 2.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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Alternative splicing.
KW NON_TER 1
FT DOMAIN 1 105 CH1.
FT DOMAIN 106 217 CH2.
FT DOMAIN 218 324 CH3.
FT DOMAIN 325 436 CH4.
FT DOMAIN 437 455
FT DISULFID 14 14
FT DISULFID 28 89
FT DISULFID 136 199
FT DISULFID 216 216
FT DISULFID 246 305
FT DISULFID 293 293
FT DISULFID 353 415
FT DISULFID 454 454
FT CARBOHYD 46 46
FT CARBOHYD 211 211
FT CARBOHYD 243 243
FT CARBOHYD 281 281
FT CARBOHYD 442 442
FT VARIANT 78 78
FT VARIANT 101 101
FT VARIANT 226 226
FT VARIANT 258 258
FT VARIANT 258 258
FT VARIANT 368 368
SQ SEQUENCE 455 AA; 50101 MW; 4CB57CB602F9B51 CRC64;

Query Match 24.5%; Score 455.5; DB 1; Length 455;
Best Local Similarity 32.1%; Pred. No. 2.9e-27;
Matches 105; Conservative 63; Mismatches 140; Indels 19; Gaps 8;

Qy 23 PTVKLFHSSCDPR---GDAHSTTQLCLVSGFSPAKVHVTVLVDGQEAENLF---PVT 75
Db 112 PNVNPF---VPRDGFSGPAPRKSLICEATNFTPKPTVSVLWLDGKLVESGFTDPVTI 168

Qy 76 RPREGGOTFSIQSEVNITQGMSSNTYTCVHKNGSIF-EDSSRRCSDDPRGVITVL 134
Db 169 ENKSGTPTQYKIVSTLTISEIDNLNLYTCRVDRHGTFLKNVSTCAASPSTILLFT 228

Qy 135 IPPSPDLIYENGTPKLTCLVLDLSEENITVTVRERKKSIGSASQSRSTKHHATTSTTS 194
Db 229 IPPSPADIFLSKANLTCLVSNLATYETLNISWASQSGEPLTKIKIMESHPPNGTFSAGK 288

Qy 195 ILPVDAKDWIEGEGVQCHVDHPHPKPIVRSITKLPGK--RLAPEVYMLPSPSEETG--T 250
Db 289 VASVCVEDNNRKEFVCTVTHRDLPSPQKFTISK-PNEVHKHPAPVAYLLPPAREQLNRE 347

Qy 251 TRVTCLIRGVFVPEISVQWLPPNNEEDHTGHTTTPRQKDHGTDPSFFLYSRLVKNKSIW 310
Db 348 SATVTCLVKRGSPADISVQWLQRGQLLPQEKVYTSAPNPEPGAPGFYTHSILTVTESEW 407

Qy 311 EKNLVCTCRVVHEALP---GSRITLEKS 334
Db 408 NSGETYTCVVGHEALPHLVHTERTVDKS 434

RESULT 11
MUCM MOUSE
ID MUCM MOUSE STANDARD; PRT; 476 AA.
AC P01873;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig mu chain C region membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 433-476 FROM N.A.
RX MEDLINE=8022874; PubMed=6771020;
RA Early P., Rogers J., Davis M., Calame K., Bond M., Wall R.,
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SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811BF208E7A CRC64;
Query Match 24.3%; Score 451.5; DB 1; Length 327;
Best Local Similarity 34.3%; Pred. No. 3.9e-27;
Matches 111; Conservative 62; Mismatches 120; Indels 31; Gaps 11;
QY 35 RGDASTIQLCLVSGFSPAKVHVTM---LVDGQEAENLFPYTRPKREGGQTFSLQSE 90
DB 16 RSTSESTALGCLVXDYPPEVTVSNWNSGALTSQ---VHTFPAVL-----QSSGLYLSLV 68
QY 91 VNITQGMSSNTYCHVKNHSGIFEDSSRRSCDDPE-----RGVITYLIPSP 139
DB 69 VTVPESS-LGTYTYCNDVHKSNKVDKVESKYPCCPCAPAEFLGGPSVFLPPKP 127
QY 140 LD-LVENGTPKLTCLVLDLSESE-NITVWVRERKKSIGSASQRTKHHTATSTISILP 197
DB 128 KOTLMISRTPEVTCVVDVSDPEQVFNWYVDGVEVHNKTKPREQPNSTYRVSVLT 187
QY 198 VDAKMWIEGGQCVDRHDPFKPIVRSITKLPKRLAPEVVMPLPSPPEE-TGTTTRVTC 256
DB 188 VLUQDWLNGKEYKCKVSNKGLPSSLEKTLISKAKQPREQVTLPPSOEMTKNQVSLTC 247
QY 257 LIRGYPSEISVQWLPNNBEDTGHHTTTRPKQDHTGTPSPFELYSRMLVKNKSIWEKGNLV 316
DB 248 LVKGFPSDIAVEMESNGOPEN--NYKTTTPVLD--SDGSFELYSLTLVDKSRWQEGNVF 303
QY 317 TCRVVEALPGSRTLEKSLHYSAG 340
DB 304 SCVMHEALHNYT-QKSLSLSLG 326
RESULT 13
MUC SUNMU STANDARD; PRT; 457 AA.
AC P20768;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig mu chain C region.
OS Suncus murinus (House shrew) (Musk shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Soricidae; Crocidurinae; Suncus.
OX NCBI_TaxID=9378;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=892321144; PubMed=2497033;
RA Ishiguro H., Ichihara Y., Namikawa T., Nagatsu T., Kurosawa Y.;
RT "Nucleotide sequence of Suncus murinus immunoglobulin mu gene and
RL comparison with mouse and human mu genes.";
FEBS Lett. 247:317-322(1989).
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EMBL; X13920; CAA32113.1; ALT_INIT.
DR PIR; S03961; S03961.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00410; Ig like; 1.
DR SMART; SM00407; Igcl; 3.
DR PROSITE; PS00290; IG MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON TER 1 105
FT DOMAIN 1 105 CH1.
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FT DOMAIN 106 220 CH2.
FT DOMAIN 221 326 CH3.
FT DOMAIN 327 457 CH4.
FT DISULFID 13 13 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
FT DISULFID 27 89 BY SIMILARITY.
FT DISULFID 136 200 BY SIMILARITY.
FT DISULFID 217 217 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 248 307 BY SIMILARITY.
FT DISULFID 295 295 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 355 417 BY SIMILARITY.
FT DISULFID 456 456 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 444 444 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 457 AA; 50074 MW; 56C8C086DA4462E9 CRC64;
Query Match 24.2%; Score 449.5; DB 1; Length 457;
Best Local Similarity 29.9%; Pred. No. 8.3e-27;
Matches 100; Conservative 76; Mismatches 138; Indels 21; Gaps 8;
QY 21 IPTVTKLPHSSCDPR---GDAHSTIQLCLVSGFSPAKVHVTWLVLDGQEAENLFPYTT- 75
DB 110 LPPNVISF---VPRNPSFGNHPRTSQLICQASGSPRTIVMSWMLQRCPEVPQPSLVSTSA 166
QY 76 ---RPKREGGQTFSLQSEVNITQGMSSNTYTCHVKNHSGIFED---SSRRCSDDEPRGV 130
DB 167 VEAPKPGSGPTTFRVISRLTITENELWSQREFTQALHKGLTKFNKSVSCMGDDTSTGI 226
QY 131 ITYLIPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQRTKHHTAT 190
DB 227 SVFLLPPTFANIFLTQSAQLTCLVTLATYDLSISWRSQNGEALQTHVNISESHPNSTF 286
QY 191 SITSLIPVDKADWIEGGYQCRVDHPHPKPIVRSITKLPKRLA---PEVVMPLPSPPEE 247
DB 287 TAKGHASVCREWESGEKFTCTVQHSDLPSLPKQSLSR--PKVDANDPPSVFLVPAQEQ 344
QY 248 --TGTRTVTCLIRGFYPSSEISVQWLPNNEDHTGHHTTTPKQDKHGTDPSPFLYSRMLV 305
DB 345 LKLRESASITCLVDFSPDPVQVQWQHGGQVPDPKHYVTSNPTPEPQNPGLYFVHSILTV 404
QY 306 NKSIWEKGNLVTCTRVHVEALPGSRTLEKSLHYSAG 340
DB 405 SEKOWSSGESFSVCVVGHEALPLSVT-EKAVDKTSG 438
RESULT 14
GCL_HUMAN STANDARD; PRT; 330 AA.
ID GCL_HUMAN
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=62274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=3489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
```


Db 58 --QSSGLYSLSSVTVTPSS--LGTYQICNVNHNKPSNTKVDKKVPEKSCDKTHTTCCPCA 114
Qy 124 DDEPRGVITYLPPSPDL-LYNGTPKTLCLVLESEB-NITVTWVRERKKSIGASQR 181
Db 115 PELLGPGSVFLFPKPKOTLMSRTEPTCVVVDVSHEDPEVKFNWYDGVVHNKTKP 174
Qy 182 SPKHHHTTSSILPVDADKOWIEGEGYOCRVDPHFPKPIVRSITKLPGRKLAPEVYML 241
Db 175 REEQNSTYRVSVTLVHLQDWLNGKEYCKVSNKALPAPIBKTISKAGQPREFQVYL 234
Qy 242 PPSPEE-TGTRTAVTCLIRGFYPSISVQWLPNNBEDHTGHHTTRPQKHGTDPSPFLY 300
Db 235 PSRDELTKNQVSLCLVKGFYPSDIAVWESNGQPEN--NYKTTTPVLD--SDGSFFLY 290
Qy 301 SRMLVNSIWEKGNLVTCTVGVHVALPGSRTEKSLHYSAG 340
Db 291 SKLTVDKSRWQGNVFCVSMVHEALHNYHT-QKSLSLSPG 329

RESULT 15
MUC_MESAU
ID MUC_MESAU STANDARD; PRT; 454 AA.
AC P06337;
DT 01-JAN-1998 (Rel. 06, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig mu chain C region.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85297761; PubMed=2994005;
RA McGuire K.L., Duncan W.R., Tucker P.W.;
RT "Phylogenetic conservation of immunoglobulin heavy chains: direct
RL comparison of hamster and mouse Cmu genes."
Nucleic Acids Res. 13:5611-5628(1985).
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DR EMBL; X02804; CAA26574.1; -.
DR PIR; A02168; MHHY.
DR HSSP; P01854; LIGE.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00410; Ig_like; 2.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 105
FT DOMAIN 1 105
FT CH1.
FT DOMAIN 106 218
FT CH2.
FT DOMAIN 219 324
FT CH3.
FT DOMAIN 325 454
FT CH4.
FT DISULFID 13 13 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
FT DISULFID 13 13 BY SIMILARITY.
FT DISULFID 27 88 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 135 198 BY SIMILARITY.
FT DISULFID 215 215 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 245 304 BY SIMILARITY.
FT DISULFID 292 292 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 352 414 BY SIMILARITY.
FT DISULFID 453 453 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT CARBOHYD 45 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 454 AA; 50196 MW; 4DA2134612BE1469 CRC64;
Query Match 23.3%; Score 433.5; DB 1; Length 454;
Best Local Similarity 30.7%; Pred. No. 1.3e-25;
Matches 106; Conservative 68; Mismatches 154; Indels 17; Gaps 9;
Qy 5 HHHT---LSLPESGPTIIPPTVKLFHSSCDP-RGDAHSTIQLLCLVSGSPAKVHVTV 60
Db 91 HGNNTKDLRVP-IPVVTMNPVSVFVPSRDAPSGPAPKRSLRFCEASNFSPKOITVSW 149
Qy 61 LVDGQEAENLF---PYTTRPKREGGQTFPSLOSEVNIITOGWSSNTYTCHVKHNGSIF-E 116
Db 150 LRDKFPVKSGETTEPVPEDRGSGPRTYKVISTLTITSDMLNLSVYTCRDVDRGLTFWK 209
Qy 117 DSRRCSDDEPRGVITYLPPSPDLVYENGTPKTLCLVLDLESEBENITVTWVRERKKSIG 176
Db 210 NVSSTCAASPTDIOAFPPIPSFVGIFLNKSAITLCLVTNLATYDTLNISSWSRSGEPLE 269
Qy 177 SASQBSTKHHTTSSITSLPVDADKOWIEGEGYOCRVDPHFPKPIVRSITKLPCK--RL 234
Db 270 TKTKLTESHGNTFSAIGEANVCVEDMDSGKEFVCTVTHRDLPSPQKPFISK-PREMNKT 328
Qy 235 APEVYMLPPSPPEE--TGTRTAVTCLIRGFYPSISVQWLPNNBEDHTGHHTTRPQKHG 292
Db 329 PPAYVQQLAREQILRESAVTCLVKGFSADIFVQWLQRGQPLSQDKYVTSAPMRPQ 388
Qy 293 TDPGFLLYSRMLVNKSIWEKGNLVTCTVGVHVALP---GSRTELEKS 334
Db 389 APHLVFTHSVLTVEEWNSETVTCVVGHEALPHMVTERTVDRS 433

Search completed: March 8, 2003, 07:48:38
Job time : 14 secs